

Mon Feb 23 07:48:04 2004

align1_pap

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_r2p model

Run on: February 23, 2004, 07:32:31 ; Search time 0.5 Seconds

(without alignments)
0.087 Million cell updates/sec

Title: us-10-023-182-1

Sequence: 1 ATCTCTGCGGGCCCTGACCT.....TAAACTGAGCTACGAAAA 752

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3 segs, 29 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 3 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=soft -Q=us-10-023-182-1 -DB=US10023182.pap
-SUFFIX=ptc -OUT=align1.pap -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=3 -DOCALIGN=200
-THR SCORE=ptc -THR MAX=100 -THR MIN=0 -ALIGN=3 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO XLPEXY
-NDC SCORES=0 -LONGLOG -TURNS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: US10023182.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	61	4.3	11	US-10-023-182-4
2	51	3.6	9	US-10-023-182-5
3	46	3.3	9	US-10-023-182-6

ALIGNMENTS

RESULT 1
US-10-023-182-4

; Sequence 4, Application US/10023182

; GENERAL INFORMATION:

APPLICANT: Stockert, Elisabeth; Jager, Elke;

Chen, Yao-tseng; Scanlan, Matthew;

Knuth, Alexander; Old, Lloyd J.

TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer

Associated Proteins, Uses Thereof,

Truncated Forms of NY-ESO-1, and HLA

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski, L.L.P.

STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/023,182

FILING DATE: 17-Dec-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/751,798

FILING DATE: December 29, 2000

APPLICATION NUMBER: 09/062,422

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/725,182

FILING DATE: October 3, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, Norman D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LTD 5466.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3168

TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-10-023-182-4

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Alignment Scores:
Pred. No.: 0 Length: 11
Score: 61.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.35% Indels: 0
Gaps: 0

us-10-023-182-1 (1-752) x US-10-023-182-4 (1-11)

QY 522 TCCTGTTGATGAGTACGACGAGTGTTCG 554

DB 1 SeruendewectripilemrginCysphelen 11

RESULT 2
US-10-023-182-5

; Sequence 5, Application US/10023182

; GENERAL INFORMATION:

APPLICANT: Stockert, Elisabeth; Jager, Elke;

Chen, Yao-tseng; Scanlan, Matthew;

Knuth, Alexander; Old, Lloyd J.

TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer

Associated Proteins, Uses Thereof,

Truncated Forms of NY-ESO-1, and HLA

Binding Peptides Derived Therefrom

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski, L.L.P.

STREET: 666 Fifth Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10103

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-023-182-5
Alignment Scores:
Pred. No.: 0 Length: 9
Score: 51.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
DB: 1 Gaps: 0
us-10-023-182-1 (1-752) x US-10-023-182-5 (1-9)
QY 522 TCCTGTGATGTGATCAGCAGTGC 548
Db 1 Serleuemetripierthgincys 9
RESULT 3
US-10-023-182-6
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
Chen, Yao-tseng; Scanlan, Matthew;
Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
Associated Proteins, Uses Thereof,
Truncated Forms of NY-ESO-1, and HLA
Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 Kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-023-182-6
Alignment Scores:
Pred. No.: 0 Length: 9
Score: 46.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.28% Indels: 0
DB: 1 Gaps: 0
us-10-023-182-1 (1-752) x US-10-023-182-6 (1-9)
QY 516 CAGCTTCCTGTGATGTGATCAGC 542
Db 1 Glnleuserleuemetripierthr 9
Search completed: February 23, 2004, 07:32:32
Job time: 0.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2004, 17:13:46 ; Search time 2487.52 Seconds
(without alignments)
180.906 Million cell updates/sec

Title: US-10-023-182-4
Perfect score: 61
Sequence: 1 SLIMWITCFL 11

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 segs, 2045481386 residues
Total number of hits satisfying chosen parameters: 1074678

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO.spool/US10023182/runat_20022004_111043_21319/app.query.fasta_1.597
-DB=GenEmbl -QFWT=fastcap -SUFWT=rxg -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=b1ts -START=1 -END=1 -MATRIX=b1ts62 -TRANS=human40.cdi -LIST=45
-NOALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=33
-USER=US10023182@cgn2_1.3707@runat_20022004_111043_21319 -NCPU=6 -ICPU=3
-NO_WMAP -LARGESUBQUERY -NEG.SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_scs:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pin:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	43	70.5	21	6	AX024699 Sequence
C 2	36	59.0	30	6	AX611551 Sequence
C 3	34	55.7	25	6	BD173647 Novel phy
C 4	33	54.1	24	6	AX445146 Sequence
C 5	33	54.1	24	6	AX453511 Sequence
C 6	32	52.5	19	6	AR042534 Sequence
C 7	32	52.5	25	6	AX658613 Sequence
C 8	32	52.5	30	6	AX611550 Sequence
C 9	32	52.5	30	6	AX611552 Sequence
C 10	32	52.5	30	6	AX611554 Sequence
C 11	32	52.5	30	6	AX611556 Sequence
C 12	31	50.8	21	6	AR295415 Sequence
C 13	30	49.2	23	6	BD094612 Substrate
C 14	30	49.2	25	6	AX115148 Sequence
C 15	30	49.2	25	6	AX358296 Sequence
C 16	30	49.2	26	6	AX127634 Sequence
C 17	30	49.2	31	6	AR229790 Sequence
C 18	29	47.5	20	6	AR116453 Sequence
C 19	29	47.5	20	6	AR116506 Sequence
C 20	29	47.5	20	6	AR116507 Sequence
C 21	29	47.5	20	6	AR135326 Sequence
C 22	29	47.5	20	6	BD074610 Antisense
C 23	29	47.5	20	6	BD074663 Antisense
C 24	29	47.5	20	6	BD074664 Antisense
C 25	29	47.5	21	6	AR296172 Sequence
C 26	29	47.5	21	6	AX539566 Sequence
C 27	29	47.5	21	6	AX539568 Sequence
C 28	29	47.5	22	6	AR212971 Sequence
C 29	29	47.5	22	6	AR300141 Sequence
C 30	29	47.5	22	6	AX115589 Sequence
C 31	29	47.5	23	6	BD176829 Novel p10
C 32	29	47.5	24	6	AR019465 Sequence
C 33	29	47.5	24	6	BD062672 Novel Fab
C 34	29	47.5	25	6	AR221882 Sequence
C 35	29	47.5	25	6	AX610805 Sequence
C 36	29	47.5	31	6	A84414 Sequence
C 37	29	47.5	31	6	AR279893 Sequence
C 38	29	47.5	31	6	AX427313 Sequence
C 39	29	47.5	31	6	BD082515 A method
C 40	29	47.5	32	6	AX503862 Sequence
C 41	29	47.5	32	6	BD106998 Modified
C 42	29	47.5	33	6	A39298 Sequence
C 43	29	47.5	33	6	AX133875 Sequence
C 44	29	47.5	33	6	AX727827 Sequence
C 45	28	45.9	17	6	AX727827 Sequence

RESULT 1

ALIGNMENTS

AX024699/c
 LOCUS AX024699 21 bp DNA linear PAT 15-SEP-2000
 DEFINITION Sequence 15 from Patent EP1001022.
 ACCESSION AX024699
 VERSION AX024699.1 GI:10184783
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS Aarnoudse, C.A. and Schrier, P.
 TITLE Camel, an alternative translation product of the tumour antigen
 JOURNAL
 BOEHRINGER INGELHEIM INT (DE) ; UNIV HOSPITAL LEIDEN (NL)
 FEATURES
 source
 1.21
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Primer"
 BASE COUNT 6 a 7 c 4 g 4 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.86 Length: 21
 Score: 43.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 70.49% Indels: 0
 DB: 6 Gaps: 0
 US-10-023-182-4 (1-11) x AX024699 (1-21)
 QY
 3 LeuMetTrrpIeThrgInCys 9
 Db
 21 TGGATGTGATCAGCGAGTGC 1
 RESULT 2
 AX611551/c
 LOCUS AX611551 30 bp DNA linear PAT 17-FEB-2003
 DEFINITION Sequence 2576 from Patent WO02072882.
 ACCESSION AX611551
 VERSION AX611551.1 GI:28406980
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE
 AUTHORS Cullen, P. and Seedorf, U.
 TITLE Coronary chip
 JOURNAL
 Patent: WO 02072882-A 2576 19-SEP-2002;
 OGHAM GmbH (DE)
 FEATURES
 source
 1.30
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 BASE COUNT 11 a 8 c 5 g 6 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 155 Length: 30
 Score: 36.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 66.67% Mismatches: 0
 Query Match: 59.02% Indels: 0
 DB: 6 Gaps: 0
 US-10-023-182-4 (1-11) x AX611551 (1-30)
 QY
 5 TrpIeThrgInCysPhe 10

Db
 20 TGGGTGACCTGAAGTTT 3
 RESULT 3
 BD173647/c
 LOCUS BD173647 25 bp DNA linear PAT 18-FEB-2003
 DEFINITION Novel physiologically active peptide and use thereof.
 ACCESSION BD173647
 VERSION BD173647.1 GI:28414978
 KEYWORDS
 SOURCE WO 02062996-A/2.
 ORGANISM
 REFERENCE
 AUTHORS Oaki, T., Masuda, Y., and Takatsu, Y.
 TITLE Novel physiologically active peptide and use thereof
 JOURNAL
 Patent: WO 02062996-A 2 15-AUG-2002;
 TAKEDA CHEMICAL INDUSTRIES LTD, TETSUYA OTAKI, YASUSHI MASUDA,
 YOSHIOHRO TAKATSU
 COMMENT
 OS Artificial Sequence
 PN WO 02062996-A/2
 PD 15-AUG-2002 WO 2002JP000837
 PF 01-FEB-2002 WO 2002JP000837
 PR 02-FEB-2001 JP 01P 026798
 PI TETSUYA OTAKI, YASUSHI MASUDA, YOSHIOHRO TAKATSU PC
 C12N15/12, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C07K14/PC
 47', C07K16/18, A61K45/00, A61P1/00, G01N33/15, G01N33/50, G01N33/53, PC
 C12P21/08
 CC Novel physiologically active peptide and use thereof FH Key
 FT
 FT source
 1.25
 Location/Qualifiers
 1.25
 /organism="Artificial Sequence"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 BASE COUNT 8 a 5 c 8 g 4 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 306 Length: 25
 Score: 34.00 Matches: 4
 Percent Similarity: 83.33% Conservative: 1
 Best Local Similarity: 66.67% Mismatches: 0
 Query Match: 55.74% Indels: 0
 DB: 6 Gaps: 0
 US-10-023-182-4 (1-11) x BD173647 (1-25)
 QY
 5 TrpIeThrgInCysPhe 10
 Db
 23 TGGGTGACCTGCTGCTT 6
 RESULT 4
 AX445146
 LOCUS AX445146 24 bp DNA linear PAT 03-JUL-2002
 DEFINITION Sequence 1601 from Patent WO0216649.
 ACCESSION AX445146
 VERSION AX445146.1 GI:21692424
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS Gunderson, K.
 TITLE Probes and decoder oligonucleotides
 JOURNAL
 Patent: WO 0216649-A 1601 28-FEB-2002;
 Illumina, Inc. (US)
 FEATURES
 source
 1.24
 Location/Qualifiers
 1.24
 /organism="synthetic construct"

/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
BASE COUNT 6 a 6 c 7 g 5 t
ORIGIN

Alignment Scores:

Pred. No.: 449 Length: 24
Score: 33.00 Matches: 5
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 54.10% Indels: 0
DB: 6 Gaps: 0

US-10-023-182-4 (1-11) x AX45146 (1-24)

QY 4 MetTPIleThrGlnCys 9

DB 2 ATGTGATCAGCAGCCTGC 19

RESULT 5

AX453511/c 24 bp DNA linear PAT 06-JUL-2002
LOCUS Sequence 3 from Patent WO0242440.
DEFINITION AX453511
ACCESSION AX453511 GI:21712786
VERSION
KEYWORDS
SOURCE
ORGANISM
Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; Lamiales; Solanales; Solanaceae; Petunia.

REFERENCE

1 Meyer, P.L. and Zubko, E.L.
AUTHORS
TITLE Plant growth regulation
JOURNAL Patent: WO 0242440-A 3 30-MAY-2002;
THE UNIVERSITY OF LEEDS (GB)

FEATURES

Location/Qualifiers

1..24

/organism="Petunia x hybrida"

/mol_type="genomic DNA"

/db_xref="taxon:4102"

/note="Oligonucleotide primer"

BASE COUNT 7 a 6 c 4 g 7 t

ORIGIN

Alignment Scores:

Pred. No.: 449 Length: 24
Score: 33.00 Matches: 5
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 62.50% Mismatches: 2
Query Match: 54.10% Indels: 0
DB: 6 Gaps: 0

US-10-023-182-4 (1-11) x AX453511 (1-24)

QY 2 LeuLeuMetTPIleThrGlnCys 9

DB 24 TTACTACAGTGTGATGACGACATGT 1

RESULT 6

AR042534/c 19 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 3 from patent US 581519.
DEFINITION AR042534
ACCESSION AR042534
VERSION AR042534.1 GI:5863030
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Lethe, B., Lucas, S., De Smet, C., Godelaine, D. and Boon-Falleur, T.
TITLE L1-1 tumor specific genes

JOURNAL Patent: US 581519-A 3 22-SEP-1998;
FEATURES Location/Qualifiers

SOURCE

1..19

/organism="unknown"

BASE COUNT 8 a 5 c 4 g 2 t

Alignment Scores:

Pred. No.: 554 Length: 19
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 52.46% Indels: 0
DB: 6 Gaps: 0

US-10-023-182-4 (1-11) x AR042534 (1-19)

QY 1 SerLeuLeuMetTPIle 6

DB 18 TCCTGTGTGATGTGATC 1

RESULT 7

AX658613/c 25 bp DNA linear PAT 22-MAR-2003
LOCUS Sequence 40 from Patent WO02103050.
DEFINITION AX658613
ACCESSION AX658613
VERSION AX658613.1 GI:29160940
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Hart, K.W.
AUTHORS
TITLE Virus detection method, primers therefor and screening kit
JOURNAL Patent: WO 02103050-A 40 27-DEC-2002;
University of Wales College of Medicine (GB)

FEATURES

Location/Qualifiers

1..25

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 12 a 5 c 2 g 6 t

ORIGIN

Alignment Scores:

Pred. No.: 710 Length: 25
Score: 32.00 Matches: 4
Percent Similarity: 85.71% Conservative: 2
Best Local Similarity: 57.14% Mismatches: 1
Query Match: 52.46% Indels: 0
DB: 6 Gaps: 0

US-10-023-182-4 (1-11) x AX658613 (1-25)

QY 4 MetTPIleThrGlnCysPhe 10

DB 23 ATATGGTTCATATTGTTT 3

RESULT 8

AX611550/c 30 bp DNA linear PAT 17-FEB-2003
LOCUS Sequence 2575 from Patent WO02072882.
DEFINITION AX611550
ACCESSION AX611550
VERSION AX611550.1 GI:28406979
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Cullen, P. and Seedorf, U.
TITLE Coronary chip

JOURNAL Patent: WO 02072882-A 2575 19-SEP-2002;
AUTHORS OGHAM GmbH (DE)
TITLE Location/Qualifiers
JOURNAL 1.30
FEATURES /organism="Homo sapiens"
source /mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 10 a 8 c 6 g 6 t
ORIGIN

Alignment Scores:
Pred. No.: 838 Length: 30
Score: 32.00 Matches: 4
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 52.46% Indels: 0
Gaps: 0
DB: 6

US-10-023-182-4 (1-11) x AX611550 (1-30)

QY 5 TripletThgInCysPhe 10
Db 20 TGGGCCACCTGAATGTTT 3

RESULT 9
AX611552/c 30 bp DNA linear PAT 17-FEB-2003
LOCUS AX611552
DEFINITION Sequence 2577 from Patent WO02072882.
ACCESSION AX611552
VERSION AX611552.1 GI:28406981
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Cullen, P. and Seedorf, U.
AUTHORS Coronary chip
TITLE Patent: WO 02072882-A 2577 19-SEP-2002;
JOURNAL OGHAM GmbH (DE)
FEATURES Location/Qualifiers
source 1.30
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 10 a 8 c 6 g 6 t
ORIGIN

Alignment Scores:
Pred. No.: 838 Length: 30
Score: 32.00 Matches: 4
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 52.46% Indels: 0
Gaps: 0
DB: 6

US-10-023-182-4 (1-11) x AX611552 (1-30)

QY 5 TripletThgInCysPhe 10
Db 20 TGGGCCACCTGAATGTTT 3

RESULT 10
AX611554/c 30 bp DNA linear PAT 17-FEB-2003
LOCUS AX611554
DEFINITION Sequence 2579 from Patent WO02072882.
ACCESSION AX611554
VERSION AX611554.1 GI:28406983
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Cullen, P. and Seedorf, U.
AUTHORS Coronary chip
TITLE Patent: WO 02072882-A 2579 19-SEP-2002;
JOURNAL OGHAM GmbH (DE)
FEATURES Location/Qualifiers
source 1.30
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 10 a 8 c 6 g 6 t
ORIGIN

Alignment Scores:
Pred. No.: 838 Length: 30
Score: 32.00 Matches: 4
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 52.46% Indels: 0
Gaps: 0
DB: 6

US-10-023-182-4 (1-11) x AX611554 (1-30)

QY 5 TripletThgInCysPhe 10
Db 20 TGGGCCACCTGAATGTTT 3

RESULT 12
AR295415 21 bp DNA linear PAT 12-JUN-2003
LOCUS AR295415/c
DEFINITION Sequence 7150 from patent US 6537751.
ACCESSION AR295415
VERSION AR295415.1 GI:31682699
KEYWORDS
SOURCE Unknown.

ORGANISM

Unknown.

REFERENCE 1 (bases 1 to 21)

AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.

TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome

JOURNAL Patent: US 6537751-A 7150 25-MAR-2003;

FEATURES Location/Qualifiers

source 1..21

BASE COUNT 7 a 4 c 3 g 7 t

ORIGIN

Alignment Scores:

Pred. No.: 924 Length: 21

Score: 31.00 Matches: 5

Percent Similarity: 71.43% Conservative: 0

Best Local Similarity: 71.43% Mismatches: 2

Query Match: 50.82% Indels: 0

DB: 6 Gaps: 0

US-10-023-182-4 (1-11) x AR295415 (1-21)

QY 3 LeuMetTTPleThrGlnCys 9

Db 21 CTTGATGATTAACAATTC 1

RESULT 13

BD094612 23 bp DNA linear PAT 27-AUG-2002

LOCUS Substrate for immobilizing ligand.

ACCESSION BD094612

VERSION BD094612.1 GI:22640200

KEYWORDS WO 0135098-A/50.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 23)

AUTHORS Kato, I., Izu, H. and Asada, K.

TITLE Substrate for immobilizing ligand

JOURNAL Patent: WO 0135098-A 50 17-MAY-2001;

TAKARA SHUZO CO LTD, IKUNOSHIN KATO, HIROYUKI IZU, KIYOZO ASADA

COMMENT OS Artificial Sequence

PN WO 0135098-A/50

PD 17-MAY-2001

PF 24-OCT-2000 WO 2000JP007415

PR 05-NOV-1999 JP 99P 315610

PI IKUNOSHIN KATO, HIROYUKI IZU, KIYOZO ASADA

PC GOIN13/543 GOIN13/521 GOIN13/53 GOIN13/566 GOIN13/700 CC

Designed oligonucleotide primer for amplifying a portion of CC

JNK2 gene.

FH Key Location/Qualifiers

FT source 1..23

FEATURES Location/Qualifiers

source 1..23

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

BASE COUNT 5 a 4 c 8 g 6 t

ORIGIN

Alignment Scores:

Pred. No.: 1,536+03 Length: 23

Score: 30.00 Matches: 4

Percent Similarity: 85.71% Conservative: 2

Best Local Similarity: 57.14% Mismatches: 1

Query Match: 49.18% Indels: 0

DB: 6 Gaps: 0

US-10-023-182-4 (1-11) x BD094612 (1-23)

QY 4 MetTTPleThrGlnCysPhe 10

Db 3 GATGGTGACGACGAGCTTC 23

RESULT 14 AX115148 25 bp DNA linear PAT 11-MAY-2001

LOCUS Sequence 271 from Patent WO0129262.

ACCESSION AX115148

VERSION AX115148.1 GI:14032090

KEYWORDS

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Picoult-Newburg, L. and Pohl, M.

TITLE Genotyping reagents, kits and methods of use thereof

JOURNAL Patent: WO 0129262-A 271 25-APR-2001;

Orchid Biosciences, Inc. (US)

FEATURES Location/Qualifiers

source 1..25

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="Primer"

BASE COUNT 7 a 4 c 10 g 4 t

ORIGIN

Alignment Scores:

Pred. No.: 1,656+03 Length: 25

Score: 30.00 Matches: 4

Percent Similarity: 66.67% Conservative: 0

Best Local Similarity: 66.67% Mismatches: 2

Query Match: 49.18% Indels: 0

DB: 6 Gaps: 0

US-10-023-182-4 (1-11) x AX115148 (1-25)

QY 5 TTPleThrGlnCysPhe 10

Db 19 TGGACAACTCAATGCTTC 2

RESULT 15

AX358296 25 bp DNA linear PAT 13-FEB-2002

LOCUS Sequence 5 from Patent WO0191739.

ACCESSION AX358296

VERSION AX358296.1 GI:18674950

KEYWORDS

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Wu, B., Seeley, T.W. and Williams, L.T.

TITLE Compositions and methods for treating neoplastic disease using chemotherapy and radiation sensitizers

JOURNAL Patent: WO 0191739-A 5 06-DEC-2001;

CHIRON CORPORATION (US)

FEATURES Location/Qualifiers

source 1..25

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="Antisense Oligonucleotide"

BASE COUNT 5 a 6 c 9 g 5 t

ORIGIN

Alignment Scores:

Pred. No.: 1,656+03 Length: 25

Score: 30.00 Matches: 3

Percent Similarity: 85.71% Conservative: 3

Best Local Similarity: 42.86% Mismatches: 1

Query Match: 49.18% Indels: 0

DB: 6 Gaps: 0

Mon Feb 23 07:48:04 2004

us-10-023-182-4.rge

Page 6

US-10-023-182-4 (1-11) X AX358296 (1-25)
QY 4 MetTrpIleThrGlnCysPhe 10
:::| | | | |
Db 23 CTGTGACACAGCCAGTCTAC 3

Search completed: February 21, 2004, 21:41:27
Job time : 2489.52 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2004, 13:32:10 ; Search time 209 Seconds
(without alignments)
142.076 Million cell updates/sec

Title: US-10-023-182-4
Sequence: 1 SLMTITOCPL 11

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2197996

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n model -DEV=x1h
-Q=/cgn2.1/USPTO.epool/US10023182/runat_20022004.111042.21309/app_query.fasta_1.597
-DB=N Geneseq 19Jun03 -GPMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOFCU=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blcsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pcot -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pro -NORX=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=33
-USER=US10023182 @cgn 1.1 0 @runat_20022004.111042.21309 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 19Jun03 :
1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT :
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT :
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT :
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT :
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT :
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT :
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT :
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT :
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT :
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT :
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT :
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT :
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT :
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT :
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT :
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT :
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT :
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT :
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT :
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT :
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT :
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT :
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT :
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT :
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT :

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	43	70.5	21	21	AAD00156
C 2	34	55.7	25	24	ABQ79049
C 3	34	55.7	30	24	ABX70076
C 4	34	55.7	33	24	ABK10659
C 5	33	54.1	24	24	ABK90497
C 6	33	54.1	24	24	ABQ01594
C 7	33	54.1	24	24	ABQ07119
C 8	33	54.1	24	24	ABQ07160
C 9	33	54.1	23	24	ABV75669
C 10	32	52.5	19	19	AAV50351
C 11	32	52.5	25	25	ABT31788
C 12	32	52.5	30	24	ABX68717
C 13	31	50.8	21	21	AAZ72794
C 14	31	50.8	25	25	ABD51987
C 15	31	50.8	29	15	AAV34559
C 16	31	50.8	30	20	AAZ10401
C 17	30	49.2	23	21	AAAS9821
C 18	30	49.2	23	22	AAH41803
C 19	30	49.2	25	22	AAH68714
C 20	30	49.2	25	22	AAH37475
C 21	30	49.2	25	24	AAI72246
C 22	30	49.2	26	22	AAH06451
C 23	30	49.2	29	16	AAQ94508
C 24	30	49.2	29	17	AAI38622
C 25	30	49.2	30	13	AAQ22324
C 26	30	49.2	30	20	AAH82214
C 27	30	49.2	31	19	AAV44722
C 28	30	49.2	31	22	AAV73764
C 29	29	47.5	20	20	AAK29334
C 30	29	47.5	20	20	AAK29387
C 31	29	47.5	20	20	AAK29388
C 32	29	47.5	20	21	AAK62877
C 33	29	47.5	20	21	AAK62930
C 34	29	47.5	20	21	AAK62931
C 35	29	47.5	20	21	AAK73776
C 36	29	47.5	20	22	AAK92896
C 37	29	47.5	20	25	ABK04430
C 38	29	47.5	21	21	AAK77084
C 39	29	47.5	21	21	AAK73551
C 40	29	47.5	21	24	ABK67015
C 41	29	47.5	21	24	ABK67017
C 42	29	47.5	21	25	ABK32110
C 43	29	47.5	22	21	AAK29237
C 44	29	47.5	22	21	AAK58158
C 45	29	47.5	22	21	AAK37995

ALIGNMENTS

RESULT 1
AAD00156/c
AAD00156 standard; DNA; 21 BP.

31-JUL-2000 (first entry)

Reverse PCR primer R2, for construction of PCR-464 vector.

CAMEL; CTL-recognised Antigen on MBianoma; cytotoxic T lymphocyte; CTL;
tumour-associated antigen; LAGE-1; NY-ESO-1; anticancer; melanoma; human;
cancer; immunotherapy; immune response; PCR primer; ss.

Homo sapiens.

W0200023584-A1.

XX 27-APR-2000.
XX
XX 15-OCT-1999; 99WO-EP07832.
XX
XX 16-OCT-1998; 98EP-0119583.
XX
XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX (UYHO-) UNIV HOSPITAL LEIDEN.
XX
XX Schrier FI, Aarnoudse CA, Heider K, Klade C,
XX WPI: 2000-339685/29.
XX
XX Tumor-associated antigen useful for cancer immunotherapy is encoded by
XX the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA -
XX
XX Disclosure; Page 66; 73pp; English.
XX
XX The present DNA sequence is the reverse PCR primer R2, used along with
XX forward PCR primer SP6F-PSV, to generate the deletion construct,
XX PCR-464 of CAMEL cDNA clone 4H8
XX
XX The tumour-associated antigen, CAMEL (Cytotoxic T lymphocytes (CTL)-
XX recognised Antigen on Melanoma) is encoded by the open reading frame
XX (ORF)-1 of LAGE-1 gene, a tumour-specific antigen. It shows strong
XX homology with NY-ESO-1, a tumour specific antigen. The tumour-associated
XX antigen displayed on melanoma cells is recognised by cytotoxic T
XX lymphocytes. CAMEL is expressed in tumour cell lines, tumour tissues
XX (e.g. breast and lung) and in restricted number of healthy tissues. It
XX has anticancer activity. CAMEL tumour antigen and immunogenic peptides
XX derived from it are useful for cancer immunotherapy. They have the
XX potential to induce an immune response, by eliciting a CTL response. The
XX DNA molecule is used for construction of recombinant or fusion proteins.
XX
XX Sequence 21 BP; 6 A; 7 C; 4 G; 4 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 6.22 Length: 21
XX Score: 43.00 Matches: 7
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 70.49% Indels: 0
XX DB: 21 Gaps: 0
XX
XX US-10-023-182-4 (1-11) x AAD00156 (1-21)
XX
XX QY 3 LeuMetThrGlnCys 9
XX |||||
XX DB 21 TTGATGTGATCAGCAGTGC 1
XX
XX RESULT 2
XX ABQ79049/c
XX ID ABQ79049 standard; DNA; 25 BP.
XX
XX AC ABQ79049;
XX
XX DT 15-NOV-2002 (first entry)
XX
XX DE Mouse ZAQ PCR primer mMIT1-R3.
XX
XX KW Mouse; physiological; G protein-coupled receptor; ZAQ; antidiarrheal;
XX laxative; anti-inflammatory; digestive disease; diarrhoea; constipation;
XX colitis; gene therapy; PCR; primer; ss.
XX
XX OS Mus sp.
XX
XX PN WO200262996-A1.
XX
XX PD 15-AUG-2002.
XX
XX PF 01-FEB-2002; 2002WO-JP00837.
XX
XX PR 02-FEB-2001; 2001JP-0026798.

XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Ohzeki T, Masuda Y, Takatsu Y;
XX
XX WPI: 2002-627554/67.
XX
XX Physiologically-active brain-originated G protein-coupled receptor
XX peptide ZAQ and encoding DNA, useful for developing drugs to treat
XX digestive diseases e.g. diarrhoea, constipation and colitis, including
XX gene therapy -
XX
XX Example 1; Page 109; 184pp; Japanese.
XX
XX The invention relates to a novel physiologically-active brain-originated
XX G protein-coupled receptor peptide designated ZAQ. The proteins of the
XX invention have antidiarrheic, laxative, and anti-inflammatory activity.
XX The DNA and encoded protein are useful for developing drugs for the
XX treatment of diseases of the digestive organs e.g. diarrhoea,
XX constipation and colitis. The polynucleotides may have a use in gene
XX therapy. The sequence represents a PCR primer used in the invention to
XX amplify murine ZAQ cDNA.
XX
XX Sequence 25 BP; 8 A; 5 C; 8 G; 4 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 259 Length: 25
XX Score: 34.00 Matches: 4
XX Percent Similarity: 83.33% Conservative: 1
XX Best Local Similarity: 56.67% Mismatches: 0
XX Query Match: 55.74% Indels: 0
XX DB: 24 Gaps: 0
XX
XX US-10-023-182-4 (1-11) x ABQ79049 (1-25)
XX
XX QY 5 TrypleThrGlnCysPhe 10
XX |||||
XX DB 23 TGGGTGACCTTGCTTT 6
XX
XX RESULT 3
XX ABX70076
XX ID ABX70076 standard; DNA; 30 BP.
XX
XX AC ABX70076;
XX
XX DT 07-MAY-2003 (first entry)
XX
XX DE Novel Helicobacter pylori gene PCR primer #3047.
XX
XX KW Protein-protein interaction; ulcer; selected interacting domain;
XX SID; PCR; primer; ss.
XX
XX OS Helicobacter pylori.
XX
XX PN WO200266501-A2.
XX
XX PD 29-AUG-2002.
XX
XX PF 28-DEC-2001; 2001WO-EP15428.
XX
XX PR 02-JAN-2001; 2001US-259302P.
XX
XX KW (HYBR-) HYBRIGENICS
XX (INSP) INST PASTERUR.
XX
XX Legrain P, Rain J, Colland F, De Reuse H, Labigne A;
XX WPI: 2002-674910/72.
XX
XX New complexes of protein-protein interactions in Helicobacter pylori,
XX useful for identifying modulating compounds for treating or preventing
XX ulcers in mammals -
XX

PS Example 9; Page 583; 642pp; English.

XX The invention describes a complex of protein-protein interactions in

CC Helicobacter pylori selected from 421 complexes given in the

CC specification. The complex of protein-protein interactions are useful

CC for screening for agents which modulate the interaction of proteins.

CC Modulating compounds which binds to a targeted bacterial protein may be

CC used for treating or preventing ulcers in a human or animal. This

CC sequence represents a primer used to isolate polynucleotides encoding

CC Helicobacter pylori proteins for studies on protein-protein

CC interactions.

XX

SQ Sequence 30 BP; 11 A; 8 C; 5 G; 3 T; 3 U; 0 other;

Alignment Scores:

Pred. No.:	317	Length:	30
Score:	34.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	71.43%	Mismatches:	0
Query Match:	55.74%	Indels:	0
DB:	24	Gaps:	0

US-10-023-182-4 (1-11) X ABX70076 (1-30)

OY 2 LeuMetTP1lethrgin 8

DB 5 AUCAGATGCTGATCACCACA 25

RESULT 4

ABK10659

ID ABK10659 standard; DNA; 33 BP.

XX

AC ABK10659;

XX

DT 21-MAY-2002 (first entry)

XX

DE Human renal cancer RAGE4 antigen 22 cDNA PCR primer #1.

XX

KW Human; renal cancer RAGE4 antigen 22; cancer; renal tumour; primer; ss;

KW PCR.

XX

OS Homo sapiens.

XX

PN CN1320627-A.

XX

PD 07-NOV-2001.

XX

PF 27-APR-2000; 2000CN-0115470.

XX

PR 27-APR-2000; 2000CN-0115470.

XX

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2002-131335/18.

XX

PT Polypeptide-human renal cancer RAGE4 antigen 22 and polynucleotide for

XX

PT coding it -

XX

XX Example 4; Page 17 (Disclosure); 33pp; Chinese.

XX

CC The invention relates to the human renal cancer RAGE4 antigen 22

CC polypeptide, the polynucleotide encoding it, the process for preparing

CC the polypeptide by DNA recombination and the application of the

CC polypeptide in treating diseases such as renal tumour. This sequence

CC represents a PCR primer used in cloning of cDNA encoding the human renal

CC cancer RAGE4 antigen 22 polypeptide.

XX

SQ Sequence 33 BP; 5 A; 10 C; 9 G; 9 T; 0 other;

Alignment Scores:

Pred. No.:	352	Length:	33
------------	-----	---------	----

Score: 34.00

Percent Similarity: 77.78%

Best Local Similarity: 55.56%

Query Match: 55.74%

DB: 24

Matches: 5

Conservative: 2

Mismatches: 2

Indels: 0

Gaps: 0

US-10-023-182-4 (1-11) X ABK10659 (1-33)

OY 3 LeuMetTP1lethrginCysphleu 11

DB 7 ATGATGCTGCTGACTGCTGACTCTG 33

RESULT 5

ABK90497/C

ID ABK90497 standard; DNA; 24 BP.

XX

AC ABK90497;

XX

DT 05-NOV-2002 (first entry)

XX

DE Petunia hybrida Sho-gene sequencing primer AP2.

XX

KW Sho-gene; rRNA-isopentenyl transferase; IPT; shoot development; skin;

KW senescence; harvesting; lateral branching; morphogenesis; chloroplast;

KW insect tolerance; pathogen tolerance; flood tolerance; hair; finger nail;

KW wrinkle reduction; sequencing; primer; ss.

XX

OS Petunia hybrida.

XX

PN WO200242440-A2.

XX

PD 30-MAY-2002.

XX

PF 26-NOV-2001; 2001WO-GB05175.

XX

PR 25-NOV-2000; 2000GB-0028827.

XX

PR 13-JAN-2001; 2001GB-0000971.

XX

PR 05-OCT-2001; 2001GB-0023970.

XX

PA (UTLE-) UNIV LEEDS.

XX

PI Meyer P, Zubko E;

XX

DR WPI; 2002-490204/52.

XX

PT Novel nucleic acid molecule encoding a cytokinin biosynthesis enzyme,

PT useful as cosmetic, probe and for producing plants with reduced apical

PT dominance, hormone-independent regeneration of shoot from calli and

PT leaves -

XX

PS Disclosure; Page 18; 56pp; English.

XX

CC The invention relates to a nucleic acid molecule encoding a cytokinin

CC biosynthesis enzyme (such as rRNA-isopentenyl transferase (IPT))

CC comprising a fully defined shooting gene nucleic acid sequence. The

CC sequences are useful for regulating plant growth, shoot development, cell

CC division, cell cycles, cell activity, stimulation of nutrient

CC mobilisation, delay of senescence both in vivo and post harvesting,

CC lateral branching, improvement of shelf-life, morphogenesis, increased

CC insect/pathogen tolerance and/or light initiated maturation of

CC chloroplasts. The sequences are also useful for activating target genes

CC and for regulating flood tolerance in plants. The regulation of the above

CC mentioned processes, activation of target genes or regulation of flood

CC tolerance, is carried so as to incorporate into its genome or cause to

CC tissue, plant or seed so as to incorporate into its genome or cause to

CC express above a basal level. Plant material is useful for moisturising or

CC improving condition of skin, hair, finger nails and toenails and for

CC reducing wrinkles in keratinous structures. This sequence represents a

CC primer used in sequencing analysis of Sho-gene DNA which encodes an

CC IPT-like cytokinin biosynthesis enzyme.

XX

SQ Sequence 24 BP; 7 A; 6 C; 4 G; 7 T; 0 other;

XX Oligonucleotide adapter/capture probe 7151.
 DE Oligonucleotide array; adapter sequence; probe; ss.
 XX
 KM Synthetic.
 OS
 XX WO200216649-A2.
 PN
 XX 28-FEB-2002.
 FD
 XX 27-AUG-2001; 2001WO-US26519.
 PF
 XX 25-AUG-2000; 2000US-227948P.
 PR
 XX 29-AUG-2000; 2000US-228854P.
 XX
 PA (ILU-) ILUDMINA INC.
 XX
 PI Gundersen K;
 XX
 DR WPI; 2002-292068/33.
 XX
 PT Array comprising adapter sequences useful for immobilizing or detecting
 PT a target nucleic acid sequence, has different addresses comprising
 PT different specific capture probes
 PS
 XX Claim 1; Page 177; 261pp; English.
 PS
 XX The invention relates to an oligonucleotide array (I) comprising at least
 CC 25 different addresses (adapter sequences) with each comprising a
 CC different capture probe selected from a group consisting of the sequences
 CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
 CC nucleic acid sequence by attaching a adapter nucleic acid
 CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
 CC nucleic acid and contacting the modified target nucleic acid with (I).
 CC The steps of above method is useful for detecting a target nucleic acid,
 CC which further comprises detecting the presence of the modified target
 CC nucleic acid.
 CC
 XX Sequence 24 BP; 5 A; 7 C; 6 G; 6 T; 0 other;
 SQ
 Alignment Scores:
 Pred. No.: 366 Length: 24
 Score: 33.00 Matches: 5
 Percent Similarity: 83.33% Conservative: 0
 Best Local Similarity: 83.33% Mismatches: 1
 Query Match: 54.10% Indels: 0
 DB: 24 Gaps: 0
 US-10-023-182-4 (1-11) x ABQ07160 (1-24)
 QY 4 MetTPTleThrGlnCys 9
 DB 23 ATGTGATCAGACGACTGC 6
 RESULT 9
 ABV75669
 ID ABV75669 standard; DNA; 33 BP.
 XX
 AC ABV75669;
 XX
 DT 28-JAN-2003 (first entry)
 XX
 DE Human FD16.06 PCR primer 3.
 XX
 KM Human; FD16.06; Cancer; HIV; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN CN1351034-A.
 XX
 PD 29-MAY-2002.
 XX

PF 26-OCT-2000; 2000CN-0125785.
 XX
 PR 26-OCT-2000; 2000CN-0125785.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-619857/67.
 XX
 PT polypeptide-human FD16.06 and polynucleotide for coding it, useful for
 PT treating diseases such as cancer and HIV infection -
 XX
 PS Example 4; Page 17 (Disclosure); 33pp; Chinese.
 XX
 CC The invention relates to a novel polypeptide, human FD16.06, and the
 CC polynucleotide encoding it. The antagonist against the polypeptide is
 CC also disclosed. The polypeptide is useful for treating diseases such as
 CC cancer and HIV infection. The present sequence represents a PCR primer
 CC used to amplify the human FD16.06 gene of the invention.
 CC
 XX Sequence 33 BP; 7 A; 4 C; 8 G; 14 T; 0 other;
 SQ
 Alignment Scores:
 Pred. No.: 522 Length: 33
 Score: 33.00 Matches: 5
 Percent Similarity: 70.00% Conservative: 2
 Best Local Similarity: 50.00% Mismatches: 3
 Query Match: 54.10% Indels: 0
 DB: 24 Gaps: 0
 US-10-023-182-4 (1-11) x ABV75669 (1-33)
 QY 2 LeuLeuMetTPTleThrGlnCysPheLeu 11
 DB 2 ATGCTAGCATGATGATGATGCTTTTGA 31
 RESULT 10
 AAV50351/C
 ID AAV50351 standard; cDNA; 19 BP.
 XX
 AC AAV50351;
 XX
 DT 27-OCT-1998 (first entry)
 XX
 DE Human LAGE-1 PCR primer B1E56.
 XX
 KM Human; LAGE-1; tumour associated protein; L1-1; diagnosis; tumour;
 KM PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9832855-A1.
 XX
 PD 30-JUL-1998.
 XX
 PF 27-JAN-1998; 98WO-US01445.
 XX
 PR 27-JAN-1997; 97US-0791495.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Boon-Falleur T, De Smet C, Godelaine D, Ietche B;
 PI Lucas S;
 XX
 DR WPI; 1998-427951/36.
 XX
 PT New isolated LAGE-1 tumour associated nucleic acids - used to
 PT develop products for the diagnosis and treatment of LAGE-1
 PT associated disorders, particularly tumours
 XX
 PS Example 1; Page 50; 73pp; English.

XX The present sequence represents a PCR primer for LAGE-1 tumour
CC associated protein (TAP). The present invention also describes: (1) a
CC method for treating a subject with a disorder characterised by
CC expression of a LAGE-1 nucleic acid molecule or an expression product,
CC comprising administering to the subject autologous cytolytic T cells to
CC ameliorate the disorder, where the cytolytic T cells are specific for
CC complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic
CC fragment; (2) a method for treating a subject with a disorder
CC characterised by expression of a LAGE-1 nucleic acid molecule or an
CC expression product, comprising administering a LAGE-1 TAP or an
CC immunogenic fragment to ameliorate the disorder; and (3) a method for
CC selectively enriching a population of T cells with cytolytic T cells
CC specific for a LAGE-1 TAP comprising contacting an isolated population
CC of T cells with an agent presenting a complex of a LAGE TAP or an
CC immunogenic fragment and a HLA presenting molecule to selectively
CC enrich the isolated population of T cells with the cytolytic T cells.
CC The methods and products from the present invention can be used for the
CC diagnosis and treatment of LAGE-1 associated disorders, particularly
CC tumours.

XX SQ Sequence 19 BP; 8 A; 5 C; 4 G; 2 T; 0 other;

Alignment Scores:

Pred. No.:	418	Length:	19
Score:	32.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	52.46%	Indels:	0
DB:	19	Gaps:	0

US-10-023-182-4 (1-11) x AAV50351 (1-19)

QY 1 SerleuleuMetTrpIle 6
ID |||||
DB 18 TCCTCTTGAATGTGATC 1

RESULT 11
ABT31788/c
ID ABT31788 standard; DNA; 25 BP.

XX AC ABT31788;

XX DT 01-MAY-2003 (first entry)

XX DE Virus detection related primer SEQ ID No 40.

XX KM Detecting; typing; determining; viral load per cell; integration state;
KM self-probing amplicon; carcinogen; HPV; SV40; PCR; primer; ss.

XX OS Unidentified.

XX OS WO2002103050-A2.

XX PN 27-DEC-2002.

XX PD 13-JUN-2002; 2002WO-GB02847.

XX PF 14-JUN-2001; 2001GB-0014430.

XX PR 28-MAR-2002; 2002GB-0007276.

XX PA (UYMA-) UNIV WALES COLLEGE OF MEDICINE.

XX PI Hart KM;

XX PT WPI; 2003-175245/17.

XX DR Detecting, typing, and determining viral load per cell and/or the
XX integration state of a virus, e.g. human papillomavirus, in a sample,
XX PT comprises employing polymerase chain reaction amplification using
XX self-probing amplicons -
XX Claim 50; Page 56; 82pp; English.

XX The invention relates to a novel method for detecting, typing, and
CC determining viral load per cell and/or the integration state of an animal
CC virus in a sample. The novel method comprises contacting the sample with
CC a virus self-probing amplicon, amplifying the product under conditions
CC enabling a detectable signal to be effected, separating the extension
CC product from the target sequence, allowing the virus probe to hybridise
CC to the target sequence of the product, and monitoring the signalling
CC system. The method is useful for detecting, typing and characterising the
CC presence of viruses, particularly those that have been associated with
CC carcinogenic activity in mammals, such as HPV or SV40. This
CC polynucleotide sequence represents a PCR primer used in the novel method
CC of the invention.

XX SQ Sequence 25 BP; 12 A; 5 C; 2 G; 6 T; 0 other;

Alignment Scores:

Pred. No.:	568	Length:	25
Score:	32.00	Matches:	4
Percent Similarity:	85.71%	Conservative:	2
Best Local Similarity:	57.14%	Mismatches:	1
Query Match:	52.46%	Indels:	0
DB:	25	Gaps:	0

US-10-023-182-4 (1-11) x ABT31788 (1-25)

QY 4 MetTrpIleThrGlnCysPhe 10
ID ::|||
DB 23 ATATGGGTTCACATTGTTT 3

RESULT 12
ABX68717
ID ABX68717 standard; DNA; 30 BP.

XX AC ABX68717;

XX DT 07-MAY-2003 (first entry)

XX DE Novel Helicobacter pylori gene PCR primer #1688.

XX KM Protein-protein interaction; ulcer; selected interacting domain;
KM SID; PCR; primer; ss.

XX OS Helicobacter pylori.

XX OS WO200266501-A2.

XX PN 29-AUG-2002.

XX PD 28-DEC-2001; 2001WO-EP15428.

XX PF 02-JAN-2001; 2001US-259302P.

XX PR (HYBR-) HYBRIGENICS.

XX PA (INSP) INST PASTEUR.

XX PI Legrain P, Rain J, Colland F, De Reuse H, Labigne A;

XX PT WPI; 2002-674910/72.

XX DR New complexes of protein-protein interactions in Helicobacter pylori,
XX useful for identifying modulating compounds for treating or preventing
XX ulcers in mammals -
XX Example 9; Page 540; 642pp; English.

XX The invention describes a complex of protein-protein interactions in
CC Helicobacter pylori selected from 421 complexes given in the
CC specification. The complex of protein-protein interactions are useful
CC for screening for agents which modulate the interaction of proteins.
CC Modulating compounds which binds to a targeted bacterial protein may be
CC used for treating or preventing ulcers in a human or animal. This
CC sequence represents a primer used to isolate polynucleotides encoding

CC Helicobacter pylori proteins for studies on protein-protein
CC interactions.
XX
SQ Sequence 30 BP, 11 A, 7 C, 4 G, 5 T, 3 U, 0 other;
Alignment Scores:
Pred. No.: 695 Length: 30
Score: 32.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 52.46% Indels: 0
DB: 24 Gaps: 0
US-10-023-182-4 (1-11) x ABX68717 (1-30)
Oy 1 SerLeuMetTrpIleThrGln 8
Db 3 UCAUCAUTTAATGATCACCACA 26
RESULT 13
AAZ72794/C
ID AAZ72794 standard; DNA; 21 BP.
XX
AC AAZ72794;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:7150.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PM WO954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GBST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 9; Page 1755; 2745pp; English.
XX
CC AA65654 to AA69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA65579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.

XX
SQ Sequence 21 BP, 7 A, 4 C, 3 G, 7 T, 0 other;
Alignment Scores:
Pred. No.: 692 Length: 21
Score: 31.00 Matches: 5
Percent Similarity: 71.43% Conservative: 0
Best Local Similarity: 71.43% Mismatches: 2
Query Match: 50.82% Indels: 0
DB: 21 Gaps: 0
US-10-023-182-4 (1-11) x AAZ72794 (1-21)
Oy 3 LeuMetTrpIleThrGlnCys 9
Db 21 CTTGATGATTCACAAATTGC 1
RESULT 14
AAD51987/C
ID AAD51987 standard; DNA; 25 BP.
XX
AC AAD51987;
XX
DT 02-MAY-2003 (first entry)
XX
DE Mouse Cyp3A11 promoter fragment specific primer, Cyp3A11R2.
XX
KW Transcription control element; transgenic; transgenic animal; toxicity;
KW drug metabolism; mouse; primer; promoter; Cyp3A11; ss.
XX
OS Mus sp.
XX
PM WO20028305-A2.
XX
PD 07-NOV-2002.
XX
PF 11-APR-2002; 2002MO-US11770.
XX
PR 12-APR-2001; 2001US-283534P.
XX
PA (XENO-) XENOGEN CORP.
XX
PI Zhang W, Contag P, Purchio A, Hashima S, Ma S, Nawotka K;
XX
DR WPI; 2003-120468/11.
XX
PT Identifying analytes that modulate expression of a reporter sequence
PT mediated by human or mouse transcription control elements in transgenic
PT rodent, comprises administering the analyte and monitoring expression
PT of coding sequence -
XX
PS Example 1; Page 56; 136pp; English.
XX
CC The invention relates to a method of identifying an analyte that
CC modulates expression of a reporter sequence mediated by transcription
CC control elements derived from a human CYP3A4 gene, in a transgenic,
CC living rodent. The method involves administering the analyte to the
CC rodent and monitoring expression of the sequence of interest where an
CC effect on expression indicates that the analyte affects the expression
CC of the reporter sequence. The method is useful for identifying an analyte
CC that modulates expression of a reporter sequence and in isolating and
CC identifying mouse and human transcriptional control elements associated
CC with cytochrome expression e.g. CYP3A11 and CYP3A4 respectively. The
CC cells and transgenic animals containing the expression cassette may be
CC used as models for studies involving toxicity and drug metabolism. The
CC present sequence is mouse Cyp3A11 promoter fragment specific primer
CC used in the exemplification of the invention.
XX
SQ Sequence 25 BP, 8 A, 3 C, 10 G, 4 T, 0 other;
Alignment Scores:
Pred. No.: 841 Length: 25
Score: 31.00 Matches: 4

Percent Similarity: 87.50% Conservative: 3
 Best Local Similarity: 50.00% Mismatches: 1
 Query Match: 50.82% Indels: 0
 DB: 25 Gaps: 0

US-10-023-182-4 (1-11) x AAD51987 (1-25)

QY 4 MetTrpIleThnGlnCyPheLeu 11
 DB 24 CTCTGCTCACTCAATCTCATG 1

RESULT 15

AAV34559
 ID AAV34559 standard; DNA; 29 BP.

XX AAV34559;

XX 11-SEP-1998 (first entry)

XX DE Escherichia coli RNA 3'-terminal phosphate cyclase PCR primer.

XX KM PCR primer; RNA 3'-terminal cyclase; RNA synthesis; metabolism;

XX study; mutagenic; ss.

XX Synthetic.

XX Escherichia coli.

XX W09745535-A1.

XX 04-DEC-1997.

XX 20-MAY-1997; 97MO-EP02566.

XX 24-MAY-1996; 96US-0018335.

XX (NOVS) NOVARTIS AG.

XX Filipowicz W, Geneschk P;

XX WPI; 1998-286352/25.

XX PT New isolated RNA 3'-terminal phosphate cyclase nucleic acids - used

XX CC to develop products for the study of RNA synthesis and metabolism in

XX CC cells and for detection, diagnosis and therapy

XX PS Example 2; Page 29; 71pp; English.

XX CC The sequence is that a PCR primer which was used in the

XX CC mutagenesis of RNA 3'-terminal phosphate cyclase.

XX SQ Sequence 29 BP; 6 A; 10 C; 3 G; 10 T; 0 other;

Alignment Scores: Pred. No.: 992 Length: 29

Score: 31.00 Matches: 5

Percent Similarity: 75.00% Conservative: 1

Best Local Similarity: 62.50% Mismatches: 2

Query Match: 50.82% Indels: 0

DB: 19 Gaps: 0

US-10-023-182-4 (1-11) x AAV34559 (1-29)

QY 2 LeuLeuMetTrpIleThnGlnCy 9

DB 2 TTACATCTCTGATCCTTCAATGC 25

Search completed: February 21, 2004, 19:51:57

Job time : 210 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2004, 19:28:16 ; Search time 48.1724 Seconds

(without alignments)
100.788 Million cell updates/sec

Title: US-10-023-182-4

Perfect score: 61

Sequence: 1 SLMWINGCFL 11

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Fgapop 10.0 , Fgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 583842

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1h
-O=/cgn2_1/USPFO.spool/US10023182/runat 20022004 111043 21349/app.query.fasta_1.597
-DB=Issued_Patents_NA -OPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -IOFCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR.SCOR=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=33
-USER=US10023182.0CGN 1 1 95 @runat 20022004 111043 21349 -NCPUT=6 -ICPU=3
-NO MMAP -LARGEOUTRY -NEG.SCOR=0 -WAIT -DSFBLCK=100 -IONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	32	52.5	19	1	US-08-791-495-3 Sequence 3, Appl
C 2	31	50.8	21	4	US-09-442-978-7150 Sequence 7150, Ap
C 3	31	50.8	30	4	US-09-622-8808-7 Sequence 7, Appl
C 4	30	49.2	29	3	US-08-646-265A-55 Sequence 5, Appl
C 5	30	49.2	30	1	US-07-955-718-36 Sequence 36, Appl
C 6	30	49.2	30	5	PCT-US91-05742-36 Sequence 36, Appl
C 7	30	49.2	31	4	US-09-358-683-4 Sequence 4, Appl
C 8	30	49.2	31	4	US-09-319-648-35 Sequence 35, Appl
C 9	29	47.5	20	2	US-08-910-629A-34 Sequence 34, Appl
C 10	29	47.5	20	3	US-09-287-796-34 Sequence 87, Appl
C 11	29	47.5	20	3	US-09-287-796-87 Sequence 87, Appl
C 12	29	47.5	20	3	US-09-287-796-87 Sequence 88, Appl

13	29	47.5	20	3	US-09-280-799-129	Sequence 129, App
14	29	47.5	20	3	US-09-433-694-79	Sequence 79, Appl
15	29	47.5	20	3	US-09-130-616-34	Sequence 34, Appl
16	29	47.5	20	3	US-09-130-616-87	Sequence 87, Appl
17	29	47.5	20	3	US-09-130-616-88	Sequence 88, Appl
18	29	47.5	21	4	US-09-422-978-7807	Sequence 7807, Ap
19	29	47.5	22	4	US-09-056-268A-30	Sequence 30, Appl
C 20	29	47.5	22	4	US-09-435-327A-7	Sequence 7, Appl
C 21	29	47.5	24	4	US-08-746-797-5	Sequence 5, Appl
C 22	29	47.5	24	1	US-08-927-387-5	Sequence 5, Appl
C 23	29	47.5	24	2	US-08-918-058-5	Sequence 5, Appl
C 24	29	47.5	25	3	US-09-385-259-8	Sequence 8, Appl
C 25	29	47.5	25	4	US-09-645-370-8	Sequence 8, Appl
C 26	29	47.5	31	4	US-09-417-197-29	Sequence 29, Appl
C 27	28	45.9	18	1	US-08-284-860A-5	Sequence 5, Appl
C 28	28	45.9	18	1	US-08-318-867A-3	Sequence 3, Appl
C 29	28	45.9	18	3	US-08-430-277A-3	Sequence 3, Appl
C 30	28	45.9	20	2	US-08-775-009-9	Sequence 9, Appl
C 31	28	45.9	20	3	US-09-358-683-22	Sequence 22, Appl
C 32	28	45.9	20	3	US-09-489-868A-74	Sequence 74, Appl
C 33	28	45.9	24	2	US-08-332-766A-104	Sequence 104, App
C 34	28	45.9	25	4	US-09-538-709-288	Sequence 288, App
C 35	28	45.9	26	4	US-09-142-481-5	Sequence 5, Appl
C 36	28	45.9	27	3	US-09-122-230-13	Sequence 13, Appl
C 37	28	45.9	27	3	US-08-893-654B-12	Sequence 12, Appl
C 38	28	45.9	28	3	US-08-348-548-24	Sequence 24, Appl
C 39	28	45.9	28	5	PCT-US95-15716-24	Sequence 24, Appl
C 40	28	45.9	30	3	US-09-033-055A-9	Sequence 9, Appl
C 41	28	45.9	31	1	US-07-975-528-15	Sequence 15, Appl
C 42	28	45.9	33	1	US-07-658-908A-2	Sequence 2, Appl
C 43	28	45.9	33	3	US-09-257-584-33	Sequence 33, Appl
C 44	28	45.9	33	4	US-09-462-917A-141	Sequence 141, App
C 45	27	44.3	18	1	US-08-763-502-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-791-495-3/c
Sequence 3, Application US/08791495
Patent No. 5811519
GENERAL INFORMATION:
APPLICANT: Lech, Bernard
APPLICANT: Lucac, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: IL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791.495
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 3:

```

/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 19 nucleotides
/   TYPE: nucleic acid
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/   MOLECULE TYPE: cDNA
/   HYPOTHETICAL: NO
/   ANTI-SENSE: YES
/   ORIGINAL SOURCE:
/     ORGANISM: Homo sapiens
US-08-791-495-3

Alignment Scores:
Pred. No.:      82.3      Length:      19
Score:          32.00     Matches:      6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:      52.46%      Indels:      0
DB:               1         Gaps:          0

US-10-023-182-4 (1-11) x US-08-791-495-3 (1-19)

QY      1  SerLeuMetTrpIle 6
DB      18  TCCCTGTGTGATGATC 1

RESULT 2
US-09-422-978-7150/c
/ Sequence 7150, Application US/09422978
/ Patent No. 6537751
/ GENERAL INFORMATION:
/   APPLICANT: Cohen, Daniel
/   APPLICANT: Blumenfeld, Marra
/   APPLICANT: Chumakov, Ilya
/   TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
/   FILE REFERENCE: GENSET.020CPI
/   CURRENT APPLICATION NUMBER: US/09/422,978
/   EARLIER FILING DATE: 1999-10-20
/   EARLIER APPLICATION NUMBER: US 09/298,850
/   EARLIER FILING DATE: 1999-04-21
/   EARLIER APPLICATION NUMBER: US 60/109,732
/   EARLIER FILING DATE: 1998-11-23
/   EARLIER APPLICATION NUMBER: US 60/082,614
/   EARLIER FILING DATE: 1998-04-21
/   NUMBER OF SEQ ID NOS: 11796
/   SEQ ID NO 7150
/   LENGTH: 21
/   TYPE: DNA
/   ORGANISM: Homo Sapiens
/   FEATURE:
/     NAME/KEY: primer_bind
/     LOCATION: 1..21
/   OTHER INFORMATION: upstream amplification primer 99-24936 for SEQ 3216,
US-09-422-978-7150

Alignment Scores:
Pred. No.:      137      Length:      21
Score:          31.00     Matches:      5
Percent Similarity: 71.43%  Conservative: 0
Best Local Similarity: 71.43%  Mismatches: 2
Query Match:      50.82%      Indels:      0
DB:               4         Gaps:          0

US-10-023-182-4 (1-11) x US-09-422-978-7150 (1-21)

QY      3  LeuMetTrpIleThrGlnCys 9
DB      21  CTGGAATGATGTACAATGTC 1

RESULT 3
US-09-622-880B-7/c
/ Sequence 7, Application US/096228890B
/ Patent No. 6582932

```

```

/ GENERAL INFORMATION:
/   APPLICANT: FUJIKAGE, Chino
/   APPLICANT: AZUMA, Mitsuyoshi
/   TITLE OF INVENTION: NOVEL CALPIN AND DNA ENCODING THE SAME
/   FILE REFERENCE: 2000-1125A/MMC/00177
/   CURRENT APPLICATION NUMBER: US/09/622,880B
/   CURRENT FILING DATE: 2000-08-24
/   PRIOR APPLICATION NUMBER: JP 10-049430
/   PRIOR FILING DATE: 1998-03-02
/   NUMBER OF SEQ ID NOS: 16
/   SEQ ID NO 7
/   LENGTH: 30
/   TYPE: DNA
/   ORGANISM: Artificial Sequence
/   FEATURE:
/     OTHER INFORMATION: primer
US-09-622-880B-7

Alignment Scores:
Pred. No.:      203      Length:      30
Score:          31.00     Matches:      4
Percent Similarity: 100.00%  Conservative: 2
Best Local Similarity: 66.67%  Mismatches: 0
Query Match:      50.82%      Indels:      0
DB:               4         Gaps:          0

US-10-023-182-4 (1-11) x US-09-622-880B-7 (1-30)

QY      4  MetTrpIleThrGlnCys 9
DB      21  ATATGATAACTGCTGC 4

RESULT 4
US-08-646-265A-55/c
/ Sequence 55, Application US/08646265A
/ Patent No. 6214973
/ GENERAL INFORMATION:
/   APPLICANT: OHTOMO, Toshiniko
/   APPLICANT: SATO, Koh
/   APPLICANT: TSUCHIYA, Masayuki
/   TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
/   TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
/   NUMBER OF SEQUENCES: 132
/   CORRESPONDENCE ADDRESS:
/     ADDRESSEE: Foley & Lardner
/     STREET: 3000 K Street, N.W., Suite 500
/     CITY: Washington
/     STATE: D.C.
/     COUNTRY: USA
/     ZIP: 20007-5109
/   COMPUTER READABLE FORM:
/     MEDIUM TYPE: Floppy disk
/     COMPUTER: IBM PC compatible
/     OPERATING SYSTEM: PC-DOS/MS-DOS
/     SOFTWARE: Patentin Release #1.0, Version #1.30
/   CURRENT APPLICATION DATA:
/     APPLICATION NUMBER: US/08/646,265A
/     FILING DATE: 09-SEP-1996
/     CLASSIFICATION: 435
/   PRIOR APPLICATION DATA:
/     APPLICATION NUMBER: WO PCT/JP94/01763
/     FILING DATE: 19-OCT-1994
/     PRIOR APPLICATION DATA:
/     APPLICATION NUMBER: JP 5-291078
/     FILING DATE: 19-NOV-1993
/   ATTORNEY/AGENT INFORMATION:
/     NAME: WEGNER, Harold C.
/     REGISTRATION NUMBER: 25,258
/     REFERENCE/DOCKET NUMBER: 53466/184
/     TELECOMMUNICATION INFORMATION:
/       TELEPHONE: (202) 672-5300
/       TELEFAX: (202) 672-5399
/       TELEX: 904136

```

INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-646-265A-55

Alignment Scores:
Pred. No.: 292
Score: 30.00
Percent Similarity: 100.00%
Best Local Similarity: 60.00%
Query Match: 49.18%
DB: 3
Length: 29
Matches: 3
Conservative: 2
Mismatch: 0
Indels: 0
Gaps: 0

US-10-023-182-4 (1-11) x US-08-646-265A-55 (1-29)

QY 5 TripleHelixCys 9
DB 28 TGGGTGACAGTGT 14

RESULT 5
US-07-955-718-36/C
Sequence 36, Application US/07955718
Patent No. 5580767
GENERAL INFORMATION:
APPLICANT: Cowsett, Lex M
APPLICANT: Ecker, David J
TITLE OF INVENTION: Inhibition of Influenza Viruses
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07955,718
FILING DATE: September 22, 1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA: PCT/US91/05742
APPLICATION NUMBER: 32,257
FILING DATE: August 13, 1991
PRIOR APPLICATION DATA: PCT/US91/05742
APPLICATION NUMBER: 07/567,287
FILING DATE: August 14, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISIS-0382
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-955-718-36

Alignment Scores:
Pred. No.: 303
Score: 30.00
Percent Similarity: 83.33%
Best Local Similarity: 66.67%
Query Match: 49.18%
DB: 5
Length: 30
Matches: 4
Conservative: 1
Mismatch: 1
Indels: 0
Gaps: 0

Score: 30.00
Percent Similarity: 83.33%
Best Local Similarity: 66.67%
Query Match: 49.18%
DB: 1
Matches: 4
Conservative: 1
Mismatch: 1
Indels: 0
Gaps: 0

US-10-023-182-4 (1-11) x US-07-955-718-36 (1-30)

QY 5 TripleHelixCys 10
DB 22 TGGATCAGTACTGCTTT 5

RESULT 6
PCT-US91-05742-36/C
Sequence 36, Application PC/TUS9105742
GENERAL INFORMATION:
APPLICANT: Cowsett, Lex M
APPLICANT: Ecker, David J
TITLE OF INVENTION: Inhibition of Influenza Viruses
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place--46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05742
FILING DATE: 19910813
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISIS-0359
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-34391
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US91-05742-36

Alignment Scores:
Pred. No.: 303
Score: 30.00
Percent Similarity: 83.33%
Best Local Similarity: 66.67%
Query Match: 49.18%
DB: 5
Length: 30
Matches: 4
Conservative: 1
Mismatch: 1
Indels: 0
Gaps: 0

US-10-023-182-4 (1-11) x PCT-US91-05742-36 (1-30)

QY 5 TripleHelixCys 10
DB 22 TGGATCAGTACTGCTTT 5

RESULT 7
US-09-358-683-4/C
Sequence 4, Application US/09358683
Patent No. 6200807
GENERAL INFORMATION:

APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowart
TITLE OF INVENTION: ANTISENSE MODULATION OF SHP-2 EXPRESSION
FILE REFERENCE: R15-0082
CURRENT APPLICATION NUMBER: US/09/358,683
CURRENT FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 47
SEQ ID NO: 4
LENGTH: 31
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Probe
US-09-358-683-4

Alignment Scores:
Pred. No.: 314 Length: 31
Score: 30.00 Matches: 4
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 49.18% Indels: 0
DB: 3 Gaps: 0

US-10-023-182-4 (1-11) x US-09-358-683-4 (1-31)
QY 2 LeuLeuMetTTPiLeThr 7
DB 19 ATCTTGATGTGGGTGACA 2

RESULT 8
US-09-319-648-35/c
Sequence 35, Application US/09119648
Patent No. 6451330
GENERAL INFORMATION:
APPLICANT: Hawkins, Mary
TITLE OF INVENTION: Fluorescent Nucleotide Analog Hairpin
Formation for Detection of Nucleic Acid Hybridization
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/319,648
FILING DATE: 30-Jul-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,844
FILING DATE: 13-DEC-1996
APPLICATION NUMBER: WO PCT/US97/22448
FILING DATE: 10-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pang, Carol
REGISTRATION NUMBER: 48,631
REFERENCE/DOCKET NUMBER: 015280-288100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

FEATURE:
NAME/KEY: modified_base
LOCATION: 7
OTHER INFORMATION: /mod_base= OTHER
/note= "N = 2-amino purine fluorescent nucleotide analogue"
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-319-648-35

Alignment Scores:
Pred. No.: 314 Length: 31
Score: 30.00 Matches: 4
Percent Similarity: 71.43% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 2
Query Match: 49.18% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-4 (1-11) x US-09-319-648-35 (1-31)
QY 5 TrrPleThrGlnCysPheLeu 11
DB 30 TGcCTCAGcCTTGTTCCTC 10

RESULT 9
US-08-910-629A-34
Sequence 34, Application US/08910629A
Patent No. 5877309
GENERAL INFORMATION:
APPLICANT: Robert A. McKay
APPLICANT: Nicholas M. Dean
APPLICANT: Brett Monia
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: PENTIUM
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,629A
FILING DATE: August 13, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: 1SPH-0215
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-910-629A-34

Alignment Scores:
Pred. No.: 288 Length: 20
Score: 29.00 Matches: 4

Percent Similarity: 83.33%
Best Local Similarity: 66.67%
Query Match: 47.54%
DB: 2
Gaps: 0

US-10-023-182-4 (1-11) x US-08-910-629A-34 (1-20)

QY 5 TTTTleThGlnCysPhe 10
DB 2 TGGGTGACCGCAGAGCTTC 19

RESULT 10
US-09-287-796-34
Sequence 34, Application US/09287796A
Patent No. 6133246
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
FILE REFERENCE: ISPH-0350
CURRENT APPLICATION NUMBER: US/09/287,796A
EARLIER FILING DATE: 1999-04-07
EARLIER APPLICATION NUMBER: 09/130,616
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 34
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-287-796-34

Alignment Scores:
Pred. No.: 288
Score: 29.00
Percent Similarity: 83.33%
Best Local Similarity: 66.67%
Query Match: 47.54%
DB: 3
Gaps: 0

US-10-023-182-4 (1-11) x US-09-287-796-34 (1-20)

QY 5 TTTTleThGlnCysPhe 10
DB 2 TGGGTGACCGCAGAGCTTC 19

RESULT 11
US-09-287-796-87
Sequence 87, Application US/09287796A
Patent No. 6133246
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
FILE REFERENCE: ISPH-0350
CURRENT APPLICATION NUMBER: US/09/287,796A
EARLIER FILING DATE: 1999-04-07
EARLIER APPLICATION NUMBER: 09/130,616
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
NUMBER OF SEQ ID NOS: 165

SEQ ID NO 87
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-287-796-87

Alignment Scores:
Pred. No.: 288
Score: 29.00
Percent Similarity: 83.33%
Best Local Similarity: 66.67%
Query Match: 47.54%
DB: 3
Gaps: 0

US-10-023-182-4 (1-11) x US-09-287-796-87 (1-20)

QY 5 TTTTleThGlnCysPhe 10
DB 2 TGGGTGACCGCAGAGCTTC 19

RESULT 12
US-09-287-796-88
Sequence 88, Application US/09287796A
Patent No. 6133246
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
FILE REFERENCE: ISPH-0350
CURRENT APPLICATION NUMBER: US/09/287,796A
EARLIER FILING DATE: 1999-04-07
EARLIER APPLICATION NUMBER: 09/130,616
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 88
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-287-796-88

Alignment Scores:
Pred. No.: 288
Score: 29.00
Percent Similarity: 83.33%
Best Local Similarity: 66.67%
Query Match: 47.54%
DB: 3
Gaps: 0

US-10-023-182-4 (1-11) x US-09-287-796-88 (1-20)

QY 5 TTTTleThGlnCysPhe 10
DB 2 TGGGTGACCGCAGAGCTTC 19

RESULT 13
US-09-280-799-129
Sequence 129, Application US/09280799
Patent No. 6136603
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Kariya, James G
APPLICANT: McKay, Robert
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL

```

; TITLE OF INVENTION: TRANSDUCTION
; FILE REFERENCE: ISPH-0340
; CURRENT APPLICATION NUMBER: US/09/280,799
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 129
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-280-799-129

Alignment Scores:
Pred. No.: 288      Length: 20
Score: 29.00      Matches: 4
Percent Similarity: 66.67%      Conservative: 0
Best Local Similarity: 66.67%      Mismatches: 2
Query Match: 47.54%      Indels: 0
DB: 3      Gaps: 0

US-10-023-182-4 (1-11) x US-09-280-799-129 (1-20)
QY 5 TTTleThrgInCysPhe 10
Db 3 TGGATCTTCACTGCTTC 20

RESULT 14
US-09-433-694-79
; Sequence 79, Application US/09433694
; Patent No. 6165790
; GENERAL INFORMATION:
; APPLICANT: Alexander H. Borchers
; APPLICANT: Donna T. Ward
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF P13 KINASE P55 GAMMA EXPRESSION
; FILE REFERENCE: RTS-0098
; CURRENT APPLICATION NUMBER: US/09/433,694
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-433-694-79

Alignment Scores:
Pred. No.: 288      Length: 20
Score: 29.00      Matches: 5
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 47.54%      Indels: 0
DB: 3      Gaps: 0

US-10-023-182-4 (1-11) x US-09-433-694-79 (1-20)
QY 6 lIeThrgInCysPhe 10
Db 4 ATCACACAGTGCCTTC 18

RESULT 15
US-09-130-616-34
; Sequence 34, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Montia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
```

```

; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-130-616-34

Alignment Scores:
Pred. No.: 288      Length: 20
Score: 29.00      Matches: 4
Percent Similarity: 83.33%      Conservative: 1
Best Local Similarity: 66.67%      Mismatches: 1
Query Match: 47.54%      Indels: 0
DB: 3      Gaps: 0

US-10-023-182-4 (1-11) x US-09-130-616-34 (1-20)
QY 5 TTTleThrgInCysPhe 10
Db 2 TGGGTGACGACGAGCTTC 19
```

Search completed: February 21, 2004, 22:53:53
Job time : 49.1724 secs


```
Alignment Scores:
Pred. No.: 290
Score: 33.00
Percent Similarity: 83.33%
Best Local Similarity: 83.33%
Query Match: 54.10%
DB: 11
Gaps: 0

US-10-023-182-4 (1-11) x US-09-940-185-1601 (1-24)

QY 4 MetTPIleThrGlnCys 9
DB 2 ATGTGATCAGCAGCTGC 19

RESULT 2
US-10-098-263B-115637
; Sequence 115637, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 115637
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-115637

Alignment Scores:
Pred. No.: 304
Score: 33.00
Percent Similarity: 100.00%
Best Local Similarity: 80.00%
Query Match: 54.10%
DB: 15
Gaps: 0

US-10-023-182-4 (1-11) x US-10-098-263B-115637 (1-25)

QY 5 TPIleThrGlnCys 9
DB 8 TGGGTCCGCCAGTGT 22

RESULT 3
US-10-098-263B-115638
; Sequence 115638, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 115638
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-115638

Alignment Scores:
Pred. No.: 304
Score: 33.00
Percent Similarity: 100.00%
Query Match: 54.10%
DB: 15
Gaps: 0

US-10-023-182-4 (1-11) x US-10-022-334-23 (1-20)

QY 5 TPIleThrGlnCys 9
DB 15 TGGATCAGAGATGC 1

RESULT 5
US-10-349-143-7150/C
; Sequence 7150, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marla
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Ballelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR FILING DATE: 1999-10-20
; PRIOR FILING DATE: 1999-04-22,978
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/082,614
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7150
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
```



```

FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..21
OTHER INFORMATION: upstream amplification primer 99-24936 for SEQ 3216,
US-10-349-143-7150

Alignment Scores:
Pred. No.: 561
Score: 31.00
Percent Similarity: 71.43%
Best Local Similarity: 71.43%
Query Match: 50.82%
DB: 12
Gaps: 0

US-10-023-182-4 (1-11) x US-10-349-143-7150 (1-21)

Qy 3 LeuMetTPrIeThrGlnCys 9
Db 21 CTTGAATGATTTCAATTC 1

RESULT 6
US-10-121-960C-4/C
Sequence 4, Application US/10121960C
Publication No. US20030145341A1
GENERAL INFORMATION:
APPLICANT: ZHANG, Weisheng
APPLICANT: FURCHIO, Pamela
APPLICANT: MA, Shirley
APPLICANT: HASHIMA, Sandy
APPLICANT: NAMOTKA, Kevin
TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
FILE REFERENCE: 9400-0014 / PEX-014.US
CURRENT APPLICATION NUMBER: US/10/121,960C
CURRENT FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 4
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CYP3A11R2.primr
US-10-121-960C-4

Alignment Scores:
Pred. No.: 682
Score: 31.00
Percent Similarity: 87.50%
Best Local Similarity: 87.50%
Query Match: 50.82%
DB: 13
Gaps: 0

US-10-023-182-4 (1-11) x US-10-121-960C-4 (1-25)

Qy 4 MetTPrIeThrGlnCysPheLeu 11
Db 24 CTCGTGCTCACTCAATCTCTATCTG 1

RESULT 7
US-10-098-263B-44679/C
Sequence 44679, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittleman, Michael
APPLICANT: Mittleman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIORITY APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16

```

```

NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 44679
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-44679

Alignment Scores:
Pred. No.: 682
Score: 31.00
Percent Similarity: 83.33%
Best Local Similarity: 50.00%
Query Match: 50.82%
DB: 15
Gaps: 0

US-10-023-182-4 (1-11) x US-10-098-263B-44679 (1-25)

Qy 5 TPrIeThrGlnCysPhe 10
Db 25 TGGTGACCACTGCTAC 8

RESULT 8
US-09-870-937-5/C
Sequence 5, Application US/09870937
Patent No. US20020049180A1
GENERAL INFORMATION:
APPLICANT: Wu, Bin
APPLICANT: Sealey, Todd
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEOPLASTIC DISEASE USING
TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION SENSITIZERS
FILE REFERENCE: 200130.514/PP-01623.002
CURRENT APPLICATION NUMBER: US/09/870,937
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-870-937-5

Alignment Scores:
Pred. No.: 1,02e+03
Score: 30.00
Percent Similarity: 85.71%
Best Local Similarity: 42.86%
Query Match: 49.18%
DB: 9
Gaps: 0

US-10-023-182-4 (1-11) x US-09-870-937-5 (1-25)

Qy 4 MetTPrIeThrGlnCysPhe 10
Db 23 CTCGTGACCAAGCAGTCTAC 3

RESULT 9
US-10-098-263B-56835
Sequence 56835, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittleman, Michael
APPLICANT: Mittleman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIORITY APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

```

```
/ SEQ ID NO 56835
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-56835

Alignment Scores:
Pred. No.: 1.02e+03 Length: 25
Score: 30.00 Matches: 3
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 60.00% Mismatches: 0
Query Match: 49.18% Indels: 0
DB: 15 Gaps: 0

US-10-023-182-4 (1-11) x US-10-098-263B-56835 (1-25)

QY 5 TTPleThngInCys 9
DB 3 TGGGTAAcGAGGTGT 17

RESULT 10
US-10-098-263B-68204/c
/ Sequence 68204, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ PRIOR FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 68204
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-68204

Alignment Scores:
Pred. No.: 1.02e+03 Length: 25
Score: 30.00 Matches: 4
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 49.18% Indels: 0
DB: 15 Gaps: 0

US-10-023-182-4 (1-11) x US-10-098-263B-68204 (1-25)

QY 5 TTPleThngInCysPhe 10
DB 25 TGGTCAcGAGGTGTTC 8

RESULT 11
US-10-098-263B-89291
/ Sequence 89291, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ PRIOR FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 89291
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-89291

Alignment Scores:
Pred. No.: 1.02e+03 Length: 25
Score: 30.00 Matches: 5
Percent Similarity: 85.71% Conservative: 1
Best Local Similarity: 71.43% Mismatches: 1
Query Match: 49.18% Indels: 0
DB: 15 Gaps: 0

US-10-023-182-4 (1-11) x US-10-098-263B-89291 (1-25)

QY 1 SerLeuLeuMetTPleThr 7
DB 5 TCTCTCCTCGAGGTGTGACT 25

RESULT 12
US-10-098-263B-89292
/ Sequence 89292, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ PRIOR FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 89292
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-89292

Alignment Scores:
Pred. No.: 1.02e+03 Length: 25
Score: 30.00 Matches: 5
Percent Similarity: 85.71% Conservative: 1
Best Local Similarity: 71.43% Mismatches: 1
Query Match: 49.18% Indels: 0
DB: 15 Gaps: 0

US-10-023-182-4 (1-11) x US-10-098-263B-89292 (1-25)

QY 1 SerLeuLeuMetTPleThr 7
DB 5 TCTCTCCTCGAGGTGTGACT 25

RESULT 13
US-09-749-873-55/c
/ Sequence 55, Application US/09749873
/ Publication No. US20030023045A1
/ GENERAL INFORMATION:
/ APPLICANT: OHTOMO, Toshiniko
/ SATO, Koh
/ TSUCHIYA, Masayuki
/ TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
/ MEDULLOBLASTOMA CELLS
/ NUMBER OF SEQUENCES: 132
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/09/749,873
FILING DATE: 29-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,265
FILING DATE: 1996-09-09
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGENER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-749-873-55

Alignment Scores:
Pred. No.: 1,21e+03 Length: 29
Score: 30.00 Matches: 3
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 60.00% Mismatches: 0
Query Match: 49.18% Indels: 0
DB: 11 Gaps: 0

US-10-023-182-4 (1-11) x US-09-749-873-55 (1-29)

QY 5 TrrpleThrgInCys 9
DB 28 TGGGTGACAGAGTGT 14

RESULT 14
US-10-230-006-763
Sequence 763, Application US/10230006
Publication No. US20030191077A1
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Posnaugh, Kathy
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI
FILE REFERENCE: 400/056 (MEHB01-1110)
CURRENT APPLICATION NUMBER: US/10/230,006
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US 60/315,315
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 2678
SOFTWARE: PatentIn version 3.0
SEQ ID NO 763
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-230-006-763

Alignment Scores:
Pred. No.: 992 Length: 17
Score: 29.00 Matches: 4
Percent Similarity: 80.00% Conservative: 0
Best Local Similarity: 80.00% Mismatches: 1
Query Match: 47.54% Indels: 0
DB: 13 Gaps: 0

US-10-023-182-4 (1-11) x US-10-230-006-763 (1-17)

QY 5 TrrpleThrgInCys 9
|||||||

DB 3 UGAUACACUCCUCC 17

RESULT 15
US-10-230-006-764
Sequence 764, Application US/10230006
Publication No. US20030191077A1
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Posnaugh, Kathy
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC COND
FILE REFERENCE: 400/056 (MEHB01-1110)
CURRENT APPLICATION NUMBER: US/10/230,006
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US 60/315,315
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 2678
SOFTWARE: PatentIn version 3.0
SEQ ID NO 764
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-230-006-764

Alignment Scores:
Pred. No.: 992 Length: 17
Score: 29.00 Matches: 4
Percent Similarity: 80.00% Conservative: 0
Best Local Similarity: 80.00% Mismatches: 1
Query Match: 47.54% Indels: 0
DB: 13 Gaps: 0

US-10-023-182-4 (1-11) x US-10-230-006-764 (1-17)

QY 5 TrrpleThrgInCys 9
DB 1 UGAUACACUCCUCC 15

Search completed: February 22, 2004, 00:58:47
Job time : 267.138 secs

AA865688 19 bp mRNA linear EST 29-APR-1998
cg94108.s1 NCI CGAD K1d5 Homo sapiens CDNA clone IMAGE:145599 3'
similar to TR:Q34192 Q34192 NADH DEHYDROGENASE SUBUNIT 5. /, mRNA
sequence.

ACCESSION	AY006847
VERSION	AY006847.1
KEYWORDS	GI:3343305
SOURCE	EST.
ORGANISM	Schizosaccharomyces pombe (fission yeast)
	Schizosaccharomyces pombe
	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes

Schizosaccharomycetaceae; Schizosaccharomycetaceae;

REFERENCE 1 (bases 1 to 32)
Moriyama, M. and Mita, K.
Identification of expressed sequence tags of Schizosaccharomycetes

JOURNAL Unpublished
COMMENT Contact: Mitsunori Moriyama
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyama@nirs.go.jp

FEATURES
source 1..32

/organism="Schizosaccharomycetes pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc01028"
/seq="n minus"
/clone_id="Schizosaccharomycetes pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of Schizosaccharomycetes pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomycetes pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

BASE COUNT 12 a 3 c 3 g 14 t
ORIGIN

Alignment Scores:
Pred. No.: 1.22e+04 Length: 32
Score: 28.00 Matches: 4
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 45.90% Indels: 0
DB: 9 Gaps: 0

US-10-023-182-4 (1-11) x AU006847 (1-32)

OY 2 LeuMetTrrpIleThr 7
DB 11 ATACTGTATGATTACA 28

RESULT 4 TA239F10P 27 bp DNA linear GSS 13-DEC-2000

LOCUS T. brucei sheared genomic DNA clone 239F10, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL481728
VERSION AL481728.1 GI:11847244
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 27)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, P., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrel@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRU927/4 GYat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

REFERENCE AUTHORS
TITLE JOURNAL
COMMENT

Barrell, Oxford University Press, 1999).
Email: nh@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/
Location/Qualifiers

BASE COUNT 10 a 7 c 5 g 5 t
ORIGIN

Alignment Scores:
Pred. No.: 1.4e+04 Length: 27
Score: 27.00 Matches: 3
Percent Similarity: 83.33% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 44.26% Indels: 0
DB: 29 Gaps: 0

US-10-023-182-4 (1-11) x TA239F10P (1-27)

OY 4 MetTrrpIleThrGlnCys 9
DB 23 ATTGGGTATTCAGTGT 6

RESULT 5 AZ424567 31 bp DNA linear GSS 03-OCT-2000
LOCUS AZ424567
DEFINITION M0204B18r Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UGCGM0204B18 F, genomic survey sequence.
ACCESSION AZ424567
VERSION AZ424567.1 GI:10548580
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
1 (bases 1 to 31)
Dunn, P., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0204 row: B column: 18
Seq primer: CGTGTGTAACGACGCGCCACT
Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers

FEATURES
source 1..31

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0204B18"
/seq="n minus"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_id="Mouse 10kb plasmid UGCGM library"
/note="Vector: pMD229v. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson


```

//issue type="melanotic melanoma, high MDR (cell line)"
/lab host="DH10B (phage-resistant)"
/clone_id="N1H_MGC_49"
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a N1H_MGC
library."
BASE COUNT      5 a      12 c      6 g      9 t
ORIGIN
Alignment Scores:
Pred. No.:      1.81e+04      Length:      32
Score:          27.00      Matches:      4
Percent Similarity: 80.00%      Conservative: 0
Best Local Similarity: 80.00%      Mismatches: 1
Query Match:    44.26%      Indels:      0
DB:            12      Gaps:      0
US-10-023-182-4 (1-11) x BG762950 (1-32)
QY      5 TrrpleThrglncys 9
Db      3 TGGATCTTCAGTGC 17
RESULT 8
AZ660221/c      21 bp      DNA      linear      GSS 14-DEC-2000
LOCUS          AZ660221
DEFINITION     1M0538M09P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0538M09 F, genomic survey sequence.
ACCESSION      AZ660221
VERSION        AZ660221.1 GI:11797367
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
REFERENCE      Dunn, J., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
AUTHORS       Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL       Unpublished
COMMENT       Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
plate: 0538 row: M column: 09
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0538M09"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.

```

```

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      7 a      11 c      1 g      2 t
ORIGIN
Alignment Scores:
Pred. No.:      1.41e+04      Length:      21
Score:          26.00      Matches:      3
Percent Similarity: 80.00%      Conservative: 1
Best Local Similarity: 60.00%      Mismatches: 1
Query Match:    42.62%      Indels:      0
DB:            28      Gaps:      0
US-10-023-182-4 (1-11) x AZ660221 (1-21)
QY      5 TrrpleThrglncys 9
Db      17 TGGGTGGTCAAGT 3
RESULT 9
AU277327      24 bp      mRNA      linear      EST 02-JUL-2002
LOCUS          AU277327
DEFINITION     3', mRNA sequence.
ACCESSION      AU277327
VERSION        AU277327.1 GI:21680637
KEYWORDS       EST.
SOURCE         Bos taurus (cow)
ORGANISM       Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 24)
REFERENCE      Oishi, M., Yamada, T., Goma, H., Lejokole, H.Y., Taniguchi, Y. and
AUTHORS       Sasaki, Y.
TITLE         EST analysis of cloned bovine fetus and placenta
JOURNAL       Unpublished
COMMENT       Contact: Masahito Oishi
Graduate School of Agriculture
Kyoto University
Sakyo-ku Kitashirakawa, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-6331
Fax: 81-75-753-6340
Email: oishi@kars.jkns.kyoto-u.ac.jp.
Location/Qualifiers
1..24
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="fetus32C04"
/dev stage="fetus"
/clone_id="Cloned bovine fetus cDNA"
BASE COUNT      4 a      3 c      5 g      12 t
ORIGIN
Alignment Scores:
Pred. No.:      1.73e+04      Length:      24

```


Score: 26.00
Percent Similarity: 66.67%
Best Local Similarity: 50.00%
Query Match: 42.62%
DB: 9
Matches: 3
Conservative: 1
Mismatch: 2
Indels: 0
Gaps: 0

US-10-023-182-4 (1-11) x AU27327 (1-24)

QY 5 TTTTCTTAAATGCTTT 23
DB 6 TGGCTTTAAATGCTTT 23

RESULT 10 24 bp DNA 1linear GSS 27-APR-2001
AZ954670/c 2M0220N20F Mouse 10kb plasmid UGCM library Mus musculus genomic
LOCUS clone UGCM20220N20 F, genomic survey sequence.
DEFINITION
VERSION AZ954670.1 GI:13825897
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0220 row: N column: 20
Seq primer: GGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM20220N20"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:472114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

BASE COUNT 9 a and selected for ampicillin resistance."
ORIGIN 1 c 4 g 10 t

Alignment Scores:
Pred. No.: 1 73e+04 Length: 24
Score: 26.00 Matches: 5
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 62.50% Mismatch: 2
Query Match: 42.62% Indels: 0
DB: 28 Gaps: 0

US-10-023-182-4 (1-11) x AZ954670 (1-24)

QY 2 LeuLeuMetTrrTrrGlnCys 9
DB 24 ATTTTAAATTAATGACCAATG 1

RESULT 11 28 bp DNA 1linear GSS 20-FEB-2001
AZ811336 2M0077L18F Mouse 10kb plasmid UGCM library Mus musculus genomic
LOCUS clone UGCM20077L18 F, genomic survey sequence.
DEFINITION
VERSION AZ811336.1 GI:12979325
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0077 row: L column: 18
Seq primer: GGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM20077L18"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 10 c 5 g 8 t

Alignment Scores:

Pred. No.: 2.18e+04 Length: 28
Score: 26.00 Matches: 4
Percent Similarity: 66.67% Conservative: 0
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 42.62% Indels: 0
DB: 28 Gaps: 0

US-10-023-182-4 (1-11) x A2611336 (1-28)

Qy 4 MetTptleThrgInCys 9
20 ATGTGTCGAGACATGC 3

RESULT 12 B2765533 29 bp DNA 1linear GSS 13-MAR-2003

LOCUS SALK_131641.20.05.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_131641.20.05.x, genomic survey sequence.

ACCESSION B2765533
VERSION B2765533.1 GI:26938086

KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana
REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Predits,L., Shinn,P., Zimmerman,J., and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

TITLE Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

FEATURES
SOURCE This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At3g46620.
Class: TDNA tagged.

Location/Qualifiers
1..29
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_131641.20.05.x"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 4 a 6 c 6 g 13 t
Alignment Scores:

Pred. No.: 2.3e+04 Length: 29
Score: 26.00 Matches: 5
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 42.62% Indels: 0
DB: 29 Gaps: 0

US-10-023-182-4 (1-11) x B2765533 (1-29)

Qy 1 SerLeuMetTptle 6
5 TCATTACTCCGTGGATT 22

RESULT 13 AZ969930 31 bp DNA 1linear GSS 27-APR-2001
LOCUS 2M0242F24R Mouse 10kb plasmid U962M library Mus musculus genomic clone U962M0242F24 R, genomic survey sequence.

ACCESSION AZ969930
VERSION AZ969930.1 GI:13841157

KEYWORDS GSS.
MUS musculus (house mouse)
SOURCE Mus musculus

ORGANISM Mus musculus
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Baecorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A., and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std. Error: 0.00
Plate: 0242 Row: F column: 24
Seq primer: CACACGAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.

FEATURES
SOURCE Location/Qualifiers
1..31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U962M0242F24"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U962M library"
/note="Vector: pMD2M1, purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 7 a 9 c 6 g 9 t

ORIGIN

Alignment Scores:
Pred. No.: 2.55e+04 Length: 31
Score: 26.00 Matches: 3
Percent Similarity: 71.43% Conservative: 2
Best Local Similarity: 42.86% Mismatches: 2
Query Match: 42.62% Indels: 0
DB: 28 Gaps: 0

US-10-023-182-4 (1-11) x AZ969930 (1-31)

QY 3 LeuMetTP1eTh-GlnCys 9
DB 6 CTAAATGCTCTCGTCATGC 26

RESULT 14

AZ785127 32 bp DNA linear GSS 16-FEB-2001

AZ785127 2M028115R Mouse 10kb plasmid UGCM library Mus musculus genomic

DEFINITION clone UGCM0028115 R, genomic survey sequence.

ACCESSION

AZ785127 GI:12921557

VERSION

AZ785127.1 GI:12921557

KEYWORDS

Mus musculus (house mouse)

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Robert B. Weiss

University of Utah

Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0028 row: 1 column: 15

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 32.

Location/Qualifiers

1..32

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCM0028115"

/sex="Male"

/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCM library"

/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF19072.1), a copy-number ligated inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 5 c 12 g 11 t

ORIGIN

Alignment Scores:
Pred. No.: 2.67e+04 Length: 32
Score: 26.00 Matches: 4
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 80.00% Mismatches: 0
Query Match: 42.62% Indels: 0
DB: 28 Gaps: 0

US-10-023-182-4 (1-11) x AZ785127 (1-32)

QY 1 SerLeuMetTP 5
DB 18 TCATGTTGATGTGG 32

RESULT 15

AZ478502 20 bp DNA linear GSS 04-OCT-2000

IM0298B09R Mouse 10kb plasmid UGCM library Mus musculus genomic

DEFINITION clone UGCM0298B09 R, genomic survey sequence.

ACCESSION

AZ478502 GI:10637408

VERSION

AZ478502.1 GI:10637408

KEYWORDS

Mus musculus (house mouse)

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Robert B. Weiss

University of Utah

Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0298 row: B column: 09

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCM0298B09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCM library"

/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 5 c 5 g 7 t
ORIGIN

Alignment Scores:
Pred. No.: 1.94e+04 Length: 20
Score: 25.00 Matches: 3
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 60.00% Mismatches: 0
Query Match: 40.98% Indels: 0
DB: 28 Gaps: 0

US-10-023-182-4 (1-11) x AZ478502 (1-20)

Qy 3 LeuMetTPlleThr 7
|||::|||::|||
Db 3 TTGCTTGAGTGACC 17

Search completed: February 21, 2004, 22:51:38
Job time : 1596.72 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2004, 17:13:46 ; Search time 2035.24 Seconds
(without alignments)
180.906 Million cell updates/sec

Title: US-10-023-182-5
Perfect score: 51
Sequence: 1 SLMMITQC 9

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1074678

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=r1h
-Q=/csg2_1/USFTO.spool/US10023182/runat.20022004.111043.21319/app_query.fasta.1.597
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -IOOPL=0 -IOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blcsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=33
-USER=US10023182 @CEN 1.1.3707 @runat.20022004.111043.21319 -NCPU=6 -ICPU=3
-NO MAP -IARSEQUTERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DEV_TIMEOUT=120 -WARM_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELext=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_ptg:*
3: gb_in:*
4: gb_ov:*
5: gb_om:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_man:*
37: em_htg_vtc:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
C 1	43	84.3	21	6	AX024699 Sequence
C 2	33	64.7	24	6	AX445146 Sequence
C 3	33	64.7	24	6	AX453511 Sequence
C 4	32	62.7	19	6	AR042534 Sequence
C 5	31	60.8	21	6	AR295415 Sequence
C 6	30	58.8	30	6	AX611551 Sequence
C 7	29	56.9	22	6	AR300141 Sequence
C 8	29	56.9	22	6	AX115599 Sequence
C 9	29	56.9	24	6	AR019465 Sequence
C 10	29	56.9	24	6	BD062672 Sequence
C 11	29	56.9	33	6	A39298 Sequence
C 12	29	56.9	33	6	AX133875 Sequence
C 13	28	55.9	17	6	AX727827 Sequence
C 14	28	55.9	17	6	AX733091 Sequence
C 15	28	54.9	17	6	AX733203 Sequence
C 16	28	54.9	18	6	BD000827 Sequence
C 17	28	54.9	18	6	I50911 Sequence
C 18	28	54.9	18	6	I83439 Sequence
C 19	28	54.9	19	6	AX132523 Sequence
C 20	28	54.9	20	6	AX292910 Sequence
C 21	28	54.9	20	6	AX294372 Sequence
C 22	28	54.9	20	6	AX357552 Sequence
C 23	28	54.9	21	6	AX539566 Sequence
C 24	28	54.9	21	6	AX539568 Sequence
C 25	28	54.9	22	6	AX539567 Sequence
C 26	28	54.9	22	6	AX539569 Sequence
C 27	28	54.9	23	6	AX111234 Sequence
C 28	28	54.9	23	6	BD177725 Sequence
C 29	28	54.9	24	6	AX288277 Sequence
C 30	28	54.9	24	6	AX289739 Sequence
C 31	28	54.9	25	6	BD173647 Sequence
C 32	28	54.9	26	6	AX465553 Sequence
C 33	28	54.9	27	6	AR082630 Sequence
C 34	28	54.9	27	6	AX122657 Sequence
C 35	28	54.9	27	6	AX188489 Sequence
C 36	28	54.9	27	6	BD073121 Sequence
C 37	28	54.9	27	6	BD170171 Sequence
C 38	28	54.9	28	6	AR161714 Sequence
C 39	28	54.9	29	6	AX195469 Sequence
C 40	28	54.9	30	6	BD141788 Sequence
C 41	28	54.9	30	6	BD173670 Sequence
C 42	28	54.9	30	6	BD181739 Sequence
C 43	28	54.9	30	6	E09921 PCR primer
C 44	28	54.9	30	6	E16389 PCR primer
C 45	28	54.9	31	6	E16389 PCR primer
C 46	28	54.9	31	6	I26007 Sequence
C 47	28	54.9	31	6	I26007 Sequence

ALIGNMENTS

RESULT 1

AX024699/c
LOCUS AX024699 21 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 15 from Patent EP1001022.
ACCESSION AX024699
VERSION AX024699.1 GI:10184783
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
TITLE
JOURNAL
BOEHRINGER INGELHEIM INT (DE) ; UNIV HOSPITAL LEIDEN (NL)
PATENT: EP 1001022-A 15 17-MAY-2000;
1 age-1
Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Primer"
BASE COUNT 6 a 7 c 4 g 4 t
ORIGIN
Alignment Scores:
Pred. No.: 1.9 Length: 21
Score: 43.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.31% Indels: 0
DB: 6 Gaps: 0
US-10-023-182-5 (1-9) x AX024699 (1-21)
QY 3 LeuMetTrieThrgInCys 9
Db 21 TTGATGTGATCAAGCAGTGC 1
RESULT 2
AX445146
LOCUS AX445146 24 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1601 from Patent WO0216649.
ACCESSION AX445146
VERSION AX445146.1 GI:21692424
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
TITLE
JOURNAL
Gundersen, K.
Probes and decoder oligonucleotides
Patent: WO 0216649-A 1601 28-FEB-2002;
Illumina, Inc. (US)
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
BASE COUNT 6 a 6 c 7 g 5 t
ORIGIN
Alignment Scores:
Pred. No.: 201 Length: 24
Score: 33.00 Matches: 5
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 64.71% Indels: 0
DB: 6 Gaps: 0
US-10-023-182-5 (1-9) x AX445146 (1-24)
QY 4 MetTrieThrgInCys 9

Db 2 ATGTGATCAGACCTGC 19
RESULT 3
AX453511/c
LOCUS AX453511 24 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 3 from Patent WO0242440.
ACCESSION AX453511
VERSION AX453511.1 GI:21712786
KEYWORDS
SOURCE
ORGANISM
Petunia x hybrida
Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; Lamiales; Solanales; Solanaceae; Petunia.
REFERENCE
1
AUTHORS
TITLE
JOURNAL
Meyer, P.L. and Zubko, E.L.
Plant growth regulation
Patent: WO 0242440-A 3 30-MAY-2002;
THE UNIVERSITY OF LEEDS (GB)
Location/Qualifiers
1..24
/organism="Petunia x hybrida"
/mol_type="genomic DNA"
/db_xref="taxon:4102"
/note="oligonucleotide primer"
BASE COUNT 7 a 6 c 4 g 7 t
ORIGIN
Alignment Scores:
Pred. No.: 201 Length: 24
Score: 33.00 Matches: 5
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 62.50% Mismatches: 2
Query Match: 64.71% Indels: 0
DB: 6 Gaps: 0
US-10-023-182-5 (1-9) x AX453511 (1-24)
QY 2 LeuMetTrieThrgInCys 9
Db 24 TTACTACGTGATGACACATGT 1
RESULT 4
AR042534/c
LOCUS AR042534 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5811519.
ACCESSION AR042534
VERSION AR042534.1 GI:5963030
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 19)
AUTHORS
TITLE
JOURNAL
Leche, B., Lucas, S., De Smet, C., Godelaine, D. and Boon-Falleur, T.
L1-1 tumor specific genes
Patent: US 5811519-A 3 22-SEP-1998;
Location/Qualifiers
1..19
/organism="unknown"
BASE COUNT 8 a 5 c 4 g 2 t
ORIGIN
Alignment Scores:
Pred. No.: 257 Length: 19
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 62.75% Indels: 0
DB: 6 Gaps: 0
US-10-023-182-5 (1-9) x AR042534 (1-19)

Qy 1 Serleuemetriple 6
Db 18 TCCTGTGATGGATC 1

RESULT 5
AR295415/c AR300141/c 21 bp DNA linear PAT 12-JUN-2003
LOCUS AR295415 Sequence 7150 from patent US 6537751.
DEFINITION AR295415
ACCESSION AR295415
VERSION AR295415.1 GI:31682699
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Bacterial markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7150 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"

BASE COUNT 7 a 4 c 3 g 7 t
ORIGIN

Alignment Scores:
Pred. No.: 443 Length: 21
Score: 31.00 Matches: 5
Percent Similarity: 71.43% Conservative: 0
Best Local Similarity: 71.43% Mismatches: 2
Query Match: 60.78% Indels: 0
DB: Gaps: 0

US-10-023-182-5 (1-9) x AR295415 (1-21)
Qy 3 LeuemetripleThrgInCys 9
Db 21 CTGATGATGATTCATAATTGC 1

RESULT 6
AX611551/c AX611551 30 bp DNA linear PAT 17-FEB-2003
LOCUS AX611551 Sequence 2576 from Patent WO02072882.
DEFINITION AX611551
ACCESSION AX611551
VERSION AX611551.1 GI:28406980
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Cullen, P. and Seedorf, U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 2576 19-SEP-2002;
OGHAM GmbH (DE)
FEATURES Location/Qualifiers
source 1..30
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 11 a 8 c 5 g 6 t
ORIGIN

Alignment Scores:
Pred. No.: 960 Length: 30
Score: 30.00 Matches: 3
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 60.00% Mismatches: 0
Query Match: 58.82% Indels: 0
DB: Gaps: 0

US-10-023-182-5 (1-9) x AX611551 (1-30)

Qy 5 TripleThrgInCys 9
Db 20 TGGATCAGTCAATGT 6

RESULT 7
AR300141/c AR300141 22 bp DNA linear PAT 12-JUN-2003
LOCUS AR300141 Sequence 7 from patent US 6537766.
DEFINITION AR300141
ACCESSION AR300141
VERSION AR300141.1 GI:31687460
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Uckun, F.M. and Croty, M.L.
TITLE Ikarcos isoforms and mutants
JOURNAL Patent: US 6537766-A 7 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"

BASE COUNT 5 a 4 c 8 g 5 t
ORIGIN

Alignment Scores:
Pred. No.: 1.15e+03 Length: 22
Score: 29.00 Matches: 4
Percent Similarity: 80.00% Conservative: 0
Best Local Similarity: 80.00% Mismatches: 1
Query Match: 56.86% Indels: 0
DB: Gaps: 0

US-10-023-182-5 (1-9) x AR300141 (1-22)
Qy 5 TripleThrgInCys 9
Db 20 TGGATCAGTCAATGT 6

RESULT 8
AX115599/c AX115599 22 bp DNA linear PAT 11-MAY-2001
LOCUS AX115599 Sequence 722 from Patent WO0129262.
DEFINITION AX115599
ACCESSION AX115599
VERSION AX115599.1 GI:14032541
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 722 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES Location/Qualifiers
source 1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 6 a 7 c 4 g 5 t
ORIGIN

Alignment Scores:
Pred. No.: 1.15e+03 Length: 22
Score: 29.00 Matches: 3
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 60.00% Mismatches: 0
Query Match: 56.86% Indels: 0
DB: Gaps: 0

US-10-023-182-5 (1-9) x AX115599 (1-22)

Qy 5 TripleThrgInCys 9

Db 16 TGGGTACTAGTGTGC 2

RESULT 9
AR019465/c 24 bp DNA linear PAT 05-DEC-1998
LOCUS AR019465 Sequence 5 from patent US 5783432.
DEFINITION AR019465
ACCESSION AR019465 GI:3974579
VERSION AR019465.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Gentry,D.Robert., Lonsdale,J.Timothy., Payne,D.John. and
Pearson,S.Campbell.
TITLE FabH
JOURNAL Patent: US 5783432-A 5 21-JUL-1998;
FEATURES
source 1. .24
Location/Qualifiers
/organism="unknown"

BASE COUNT 8 a 6 c 3 g 7 t

ORIGIN

Alignment Scores:
Pred. No.: 1.24e+03 Length: 24
Score: 29.00 Matches: 4
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 56.86% Indels: 0
DB: 6 Gaps: 0

US-10-023-182-5 (1-9) x AR019465 (1-24)

QY 2 LeuLeuMetTPIleThrGlnCys 9
Db 24 GTAATCATGTGTGACACACTTGT 1

RESULT 10
BD062672/c 24 bp DNA linear PAT 27-AUG-2002
LOCUS BD062672 Novel FabH.
DEFINITION BD062672
ACCESSION BD062672.1 GI:22608275
VERSION BD062672.1
KEYWORDS JP 2001505050-A/4.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus
REFERENCE
AUTHORS Gentry,D.R., Lonsdale,J.T., Payne,D.J. and Pearson,S.C.
TITLE Novel FabH
JOURNAL Patent: JP 2001505050-A 4 17-APR-2001;
COMMENT
SMITHKLINE BEECHAM CORP
PN JP 2001505050-A/4
PD 17-APR-2001
PF 23-OCT-1997 JP 1998519641
PR 23-OCT-1996 US 60/028089, 18-NOV-1996 US 08/746797 PI
DANIEL ROBERT GENTRY, JOHN TIMOTHY LONSDALE, DAVID JOHN PAYNE, PI
STEWART CAMPBELL PEARSON
PC C12N1/00, C12N5/10, C12N9/10, C12N15/54, C12N15/63 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers

FEATURES
source 1. .24
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"

BASE COUNT 8 a 6 c 3 g 7 t

ORIGIN

Alignment Scores:
Pred. No.: 1.24e+03 Length: 24
Score: 29.00 Matches: 4
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 56.86% Indels: 0
DB: 6 Gaps: 0

US-10-023-182-5 (1-9) x BD062672 (1-24)

QY 2 LeuLeuMetTPIleThrGlnCys 9
Db 24 GTAATCATGTGTGACACACTTGT 1

RESULT 11
A39298 33 bp DNA linear PAT 05-MAR-1997
LOCUS A39298 Sequence 23 from Patent WO9413799.
DEFINITION A39298
ACCESSION A39298 GI:2295659
VERSION A39298.1
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS 1 (bases 1 to 33)
Hadingham,K.L. and Whiting,P.J.
TITLE STABLY TRANSFECTED CELL LINES EXPRESSING GABA-A RECEPTORS
JOURNAL Patent: WO 9413799-A 23 23-JUN-1994;
COMMENT MERCK SHARP & DOHME (GB)
Other publication CA 2151236 940623
Other publication AU 5655494 940704
Other publication JP 8504330T 960514.
FEATURES
source 1. .33
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT 14 a 4 c 6 g 9 t

ORIGIN

Alignment Scores:
Pred. No.: 1.65e+03 Length: 33
Score: 29.00 Matches: 5
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 62.50% Mismatches: 2
Query Match: 56.86% Indels: 0
DB: 6 Gaps: 0

US-10-023-182-5 (1-9) x A39298 (1-33)

QY 1 SerLeuLeuMetTPIleThrGln 8
Db 7 AGCTTGATGTAATGTGACACTACAA 30

RESULT 12
AX133875 33 bp DNA linear PAT 15-MAY-2001
LOCUS AX133875
DEFINITION Sequence 61 from Patent WO0119856.
ACCESSION AX133875
VERSION AX133875.1 GI:14139827
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Shinkens,R.A., Fernandes,E., Herrmann,J.L., Liu,X., Yang,M. and
Boldog,F.L.
TITLE Secreted human proteins, polynucleotides encoding them and methods
JOURNAL of using the same
Curagen Corporation (US)
Patent: WO 0119856-A 61 22-MAR-2001;
FEATURES
source 1. .33
Location/Qualifiers


```

BASE COUNT      5 a          9 c          10 g          9 t
ORIGIN

```

Alignment Scores:	
Pred. No.:	1.65e+03
Score:	29.00
Percent Similarity:	100.00%
Best Local Similarity:	50.00%
Query Match:	56.86%
DB:	6
	Gaps: 0
	Length: 33
	Matches: 3
	Conservative: 3
	Mismatches: 0
	Indels: 0
	Gaps: 0

US-10-023-182-5 (1-9) x AX133875 (1-33)

QY	4	MetTryptLeThrgLncys	9
	::: ::: ::: ::: :::		
Db	13	GTGTGGCTGACCAAGTGT	30

RESULT 13
AXT27827/c
17 MAY 2003

LOCUS	AX727827	17 bp	DNA
DEFINITION	Sequence 5514 from Patent WO03025176.		
ACCESSION	AX727827		
VERSION	AX727827.1	GI:30507170	

SOURCE Mus musculus (house mouse)

REFERENCE
AUTHORS
TITLE

1
Teleman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour

JOURNAL Patent: WO 03025176-A 5514 27-MAR-2003
 FEATURES Molecular Engines Laboratories (FR)
 source location/Qualifiers
 1. .17

```

BASE COUNT      6 a      3 c      5 g      3 t
ORIGIN
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

```

Alignment Scores:	
Pred. No.:	1.43e+03
Score:	28.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	54.90%
DB:	6
Gaps:	0
Length:	17
Matches:	5
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-023-182-5 (1-9) x AX727827 (1-17)

Qy 2 LeuLeuMetTrpIle 6
Db 15 CTCCTCATGTGATC 1

RESULT 14

LOCUS	17 bp	DNA	linear	PAT 08-MAY-2003
AX733091				
DEFINITION	Sequence 4725 from Patent WO03025175.			

VERSION AX733091.1 GI:30512434

SOURCE ORGANISM	Homo sapiens (human)
Homo sapiens	

REFERENCE
1 Mammalia; Eutheria; Primates; Catarrhini; Hominae; Homo.

AUTHORS Teletman, A., Amson, R. and Tufinder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 4725 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source location/Qualifiers 1 17

JOURNAL
Patent: WO 03025175-A 4725 27-MAR-2003
Molecular Engines Laboratories (EP)

FEATURES	Location/Qualifiers
source	1. .17

BASE COUNT	2 a	-	2 c	6 g	7 t
ORIGIN					

Alignment Scores:

Pred. No.:	1,43e+03	Length:	17
Score:	28.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	54.90%	Indels:	0
DB:		Gaps:	0

US-10-023-182-5 (1-9) X AX733091 (1-17)

```

QY      1 SerLeuLeuMetTrp 5
         |||||
Db      3 TCTTTGCTGATGTGG 17

```

RESULT 15
AX733203/C

DATE 06 MAY 2003

DEFINITION	Sequence	4837	from Patent	WO03025175.
ACCESSION	AX733203			
VERSION	AX733203.1	GI:30512546		

SOURCE	Homo sapiens (human)
...	...

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1
AUTHORS
Telerman, A., Amson, R. and Tuijinder, M.
TITLE
Sequences involved in phenomena of tumour suppression, tumour

JOURNAL Patent: WO 03025175-A 4837 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers

```

source      1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

BASE COUNT  7 a      4 c      3 g      3 t
ORIGIN

```

Alignment Scores:

Pred. No.:	1.43e+03	1
Score:	28.00	5
Percent Similarity:	100.00%	0
Best Local Similarity:	100.00%	0
Query Match:	54.90%	0
DB:	6	0
	Gaps:	0

US-10-023-182-5 (1-9) x AX733203 (1-17)

Qy	2	LeuLeuMetTyrIle	6
Db	15	CTTCTATGTGATC	1

Search completed: February 21, 2004, 21:41:29
Job time : 2037.24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: February 21, 2004, 13:32:10 ; Search time 171 Seconds

(Without alignments)
142.076 Million cell updates/sec

Title: US-10-023-182-5

Perfect score: 51

Sequence: 1 SLMMWITQC 9

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349715017 residues

Total number of hits satisfying chosen parameters: 2197996

Minimum DB seq length: 0

Maximum DB seq length: 33

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgm2.1/USPTO.SP001/US10023182/runat.20022004.111042.21309/app_query.fasta.1.597
-DB=N Geneseq.19Jun03 -OPMT=fastap -SUPFIX=ring -MINMATCH=0.1 -LOOFCIL=0
-LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NOEM=ext -HEAPSIZE=500 -MINTEN=0 -MAXLEN=33
-USBR=US10023182.@CGM_1.1.0.@runat.20022004.111042.21309 -NCPU=6 -ICPU=3
-NO_WAMP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WAMP TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELCP=6 -DELEXT=7

Database : N_Geneseq.19Jun03.*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	43	84.3	21	21	AAD00156	Reverse PCR primer
C 2	34	66.7	30	24	ABX70076	Novel Helicobacter
C 3	33	64.7	24	24	ABX30497	Petunia hybrida Sh
C 4	33	64.7	24	24	ABO01594	Oligonucleotide ad
C 5	33	64.7	24	24	ABO07119	Oligonucleotide ad
C 6	33	64.7	24	24	ABO07160	Oligonucleotide ad
C 7	32	62.7	19	19	AAV50351	Human LAGE-1 PCR p
C 8	32	62.7	30	24	ABX68717	Novel Helicobacter
C 9	32	62.7	33	24	ABX10659	Human renal cancer
C 10	31	60.8	21	21	AAZ72794	Human biallelic ma
C 11	31	60.8	29	19	AAV34559	Escherichia coli R
C 12	31	60.8	30	16	AAZ10401	PCR primer used to
C 13	30	58.8	29	16	AAQ94508	Human/murine chime
C 14	30	58.8	29	17	AAQ38622	Chimeric human/mu
C 15	30	58.8	31	17	AAV73764	Probe for human Sh
C 16	29	56.9	22	21	AAZ29237	Nested primer R2 f
C 17	29	56.9	22	21	AAZ58158	Jack bean concanav
C 18	29	56.9	22	22	AAH37926	SNP specific lower
C 19	29	56.9	22	22	ABX97428	Human NOV-associat
C 20	29	56.9	22	19	AAV29858	Streptococcus pneu
C 21	29	56.9	24	19	AAV22022	PCR primer for fun
C 22	29	56.9	33	15	AAO69137	Human GABA recepto
C 23	29	56.9	33	22	AAO51257	Forward PCR primer
C 24	29	56.9	33	24	ABL54121	Human lipase 37 PC
C 25	28	54.9	17	25	ABT39088	Tumour suppression
C 26	28	54.9	17	25	ABT39200	Cdc 25 hs ribozyme
C 27	28	54.9	19	21	AAH6155	Cdc25 hs ribozyme
C 28	28	54.9	19	22	AAH61317	Primer DRT52 for
C 29	28	54.9	20	18	AAV91763	Primer 22-c8T53 fo
C 30	28	54.9	20	18	AAV73305	Rat hepatocyte car
C 31	28	54.9	20	21	AAA87615	Human cot oncogene
C 32	28	54.9	20	22	AAH13366	Human Stp-2 antis
C 33	28	54.9	20	22	AAV73782	Capture oligonucle
C 34	28	54.9	20	24	ABT92952	Human forward PCR
C 35	28	54.9	20	24	ABT94414	Human forward PCR
C 36	28	54.9	20	24	AAV20429	Human familial bip
C 37	28	54.9	21	24	ABT58197	Human MRP-1 poly
C 38	28	54.9	21	24	ABT587015	Human MRP-1 poly
C 39	28	54.9	21	24	ABT587017	Novel human protei
C 40	28	54.9	21	25	ABX97656	Human MRP-1 poly
C 41	28	54.9	22	24	ABT67016	Human hpa cDNA Fra
C 42	28	54.9	22	24	ABT67018	Human hpa cDNA Fra
C 43	28	54.9	23	20	AAH40752	PCR primer used to
C 44	28	54.9	23	20	AAH86715	PCR primer used to
C 45	28	54.9	23	20	AAH86717	PCR primer used to

ALIGNMENTS

RESULT 1
AAD00156/c
ID AAD00156 standard; DNA; 21 BP.
AAD00156;
31-UTL-2000 (first entry)
Reverse PCR primer R2, for construction of PCR-464 vector.
CAMEL; CTL-recognised Antigen on Melanoma; cytotoxic T lymphocyte; CTL;
KM tumour-associated antigen; LAGE-1; NY-ESO-1; anticancer; melanoma; human;
KM cancer; immunotherapy; immune response; PCR primer; ss.
XX Homo sapiens.
XX OS
XX WO200023584-A1.

XX 27-APR-2000.
PD 15-OCT-1999; 99WO-EP07832.
XX 16-OCT-1998; 98EP-0115583.
PR (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX (UYHO-) UNIV HOSPITAL LEIDEN.
XX Schrier PI, Aarnoudse CA, Heider K, Klade C;
PI WPI; 2000-339685/29.
XX Tumor-associated antigen useful for cancer immunotherapy is encoded by
PT the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA -
XX Disclosure; Page 66; 73pp; English.
XX The present DNA sequence is the reverse PCR primer R2, used along with
CC forward PCR primer SP6F-PSV, to generate the deletion construct,
CC PCR-464 of CAMEL cDNA clone 4H8.
CC The tumour-associated antigen, CAMEL (Cytotoxic T lymphocytes (CTL)-
CC recognised Antigen on Melanoma) is encoded by the open reading frame
CC (ORF)-1 of LAGE-1 gene, a tumour-specific antigen. It shows strong
CC homology with NY-ESO-1, a tumour specific antigen. The tumour-associated
CC antigen displayed on melanoma cells is recognised by cytotoxic T
CC lymphocytes. CAMEL is expressed in tumour cell lines, tumour tissues
CC (e.g. breast and lung) and in restricted number of healthy tissues. It
CC has anticancer activity. CAMEL tumour antigen and immunogenic peptides
CC derived from it are useful for cancer immunotherapy. They have the
CC potential to induce an immune response, by eliciting a CTL response. The
CC DNA molecule is used for construction of recombinant or fusion proteins.
XX
SQ Sequence 21 BP; 6 A; 7 C; 4 G; 4 T; 0 other;
Alignment Scores:
Pred. No.: 2.65 Length: 21
Score: 43.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.31% Indels: 0
DB: 21 Gaps: 0
US-10-023-182-5 (1-9) x AAD00156 (1-21)
QY 3 LeuMetTTPileThrgInCys 9
DB 21 TTGATGTGATCGACGAGTGC 1
RESULT 2
ABX70076
ID ABX70076 standard; DNA; 30 BP.
XX
AC ABX70076;
XX
DT 07-MAY-2003 (first entry)
XX
DE Novel Helicobacter pylori gene PCR primer #3047.
XX
KW Protein-protein interaction; ulcer; selected interacting domain;
KM SID; PCR; primer; ss.
XX
OS Helicobacter pylori.
XX
PN WO200266501-A2.
XX
PD 29-AUG-2002.
XX
PF 28-DEC-2001; 2001WO-EP15428.
XX
PR 02-JAN-2001; 2001US-259302P.
XX

PA (HYBR-) HYBRIGENICS.
PA (INSP) INST PASTERUR.
XX
XX Legrain P, Rain U, Collard F, De Reuse H, Labigne A;
XX WPI; 2002-674910/72.
DR
XX
XX New complexes of protein-protein interactions in Helicobacter pylori,
PT useful for identifying modulating compounds for treating or preventing
PT ulcers in mammals -
XX
XX Example 9; Page 583; 642pp; English.
XX
XX The invention describes a complex of protein-protein interactions in
CC Helicobacter pylori selected from 421 complexes given in the
CC specification. The complex of protein-protein interactions are useful
CC for screening for agents which modulate the interaction of proteins.
CC Modulating compounds which binds to a targeted bacterial protein may be
CC used for treating or preventing ulcers in a human or animal. This
CC sequence represents a primer used to isolate polynucleotides encoding
CC Helicobacter pylori proteins for studies on protein-protein
CC interactions.
XX
SQ Sequence 30 BP; 11 A; 8 C; 5 G; 3 T; 3 U; 0 other;
Alignment Scores:
Pred. No.: 162 Length: 30
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 66.67% Indels: 0
DB: 24 Gaps: 0
US-10-023-182-5 (1-9) x ABX70076 (1-30)
QY 2 LeuMetTTPileThrgIn 8
DB 5 AUCAGATGTGATCGACCGAA 25
RESULT 3
ABK90497/C
ID ABK90497 standard; DNA; 24 BP.
XX
AC ABK90497;
XX
DT 05-NOV-2002 (first entry)
XX
DE Petunia hybrida Sho-gene sequencing primer AP2.
XX
KW Sho-gene; tRNA-isopentenyl transferase; IPT; shoot development; skin;
KW shooting gene; cell division; cell cycle; nutrient mobilisation; tocanail;
KW senescence; harvesting; lateral branching; morphogenesis; chloroplast;
KW insect tolerance; pathogen tolerance; flood tolerance; hair; finger nail;
KW wrinkle reduction; sequencing; primer; ss.
XX
OS Petunia hybrida.
XX
PN WO200242440-A2.
XX
PD 30-MAY-2002.
XX
DE 26-NOV-2001; 2001WO-GB05175.
XX
PF 25-NOV-2000; 2000GB-0028827.
XX
PR 13-JAN-2001; 2001GB-0000971.
XX
PR 05-OCT-2001; 2001GB-0023970.
XX
PA (UYLE-) UNIV LEEDS.
XX
PI Meyer P, Zubko E;
XX
DR WPI; 2002-490204/52.
XX

XX different specific capture probes -
PS Claim 1; Page 81; 261pp; English.
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid
CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
CC nucleic acid and contacting the modified target nucleic acid with (I).
CC The steps of above method is useful for detecting a target nucleic target,
CC which further comprises detecting the presence of the modified target
CC nucleic acid.

SQ Sequence 24 BP; 6 A; 6 C; 7 G; 5 T; 0 other;

Alignment Scores:
Pred. No.: 191 Length: 24
Score: 33.00 Matches: 5
Percent Similarity: 83.33% Conservativeness: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 64.71% Indels: 0
DB: 24 Gaps: 0

US-10-023-182-5 (1-9) x ABQ01594 (1-24)
OY 4 MetTPIeTh-GlnCys 9
DB 2 ATGTGATCATCGACCTGC 19
ABQ07119
ID ABQ07119 standard; DNA; 24 BP.
AC ABQ07119;
XX 11-JUN-2002 (first entry)
DT Oligonucleotide adapter/capture probe 7110.
DE Oligonucleotide adapter/capture probe 7110.
XX Oligonucleotide array; adapter sequence; probe; ss.
XX Synthetic.
OS WO200216649-A2.
PM 28-FEB-2002.
PD 27-AUG-2001; 2001WO-US26519.
PF 25-AUG-2000; 2000US-227948P.
PR 29-AUG-2000; 2000US-228854P.
PA (ILLU-) ILLUMINA INC.
XX Gunderson K;
PI WPI; 2002-292068/33.
DR Array comprising adapter sequences useful for immobilizing or detecting
PT a target nucleic acid sequence, has different addresses comprising
PT different specific capture probes -
PS Claim 1; Page 177; 261pp; English.
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid
CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
CC nucleic acid and contacting the modified target nucleic acid with (I).

CC The steps of above method is useful for detecting a target nucleic acid,
 CC which further comprises detecting the presence of the modified target
 CC nucleic acid.

XX Sequence 24 BP; 6 A; 6 C; 7 G; 5 T; 0 other;

Alignment Scores:

Pred. No.:	191	Length:	24
Score:	33.00	Matches:	5
Percent Similarity:	83.33%	Conservative:	0
Best Local Similarity:	83.33%	Mismatches:	1
Query Match:	64.71%	Indels:	0
DB:	24	Gaps:	0

US-10-023-182-5 (1-9) x ABQ07119 (1-24)

OY 4 MetTripleThgInCys 9

DB 2 ATGTGATCAGCAGCTGC 19

RESULT 6

ABQ07160/c

XX ID ABQ07160 standard; DNA; 24 BP.

XX AC ABQ07160;

XX DT 11-JUN-2002 (first entry)

XX DE Oligonucleotide adapter/capture probe 7151.

XX KM Oligonucleotide array; adapter sequence; probe; ss.

XX OS Synthetic.

XX FN WO200216649-A2.

XX PD 28-FEB-2002.

XX PF 27-AUG-2001; 2001WO-US26519.

XX PR 25-AUG-2000; 2000US-227948P.

XX PR 29-AUG-2000; 2000US-228854P.

XX PA (ILUW-) ILLUMINA INC.

XX PI Gunderson K;

XX DR WPI; 2002-292068/33.

XX PT Array comprising adapter sequences useful for immobilizing or detecting

XX PT a target nucleic acid sequence, has different addresses comprising

XX PT different specific capture probes -

XX PS Claim 1; Page 177; 261pp; English.

XX CC The invention relates to an oligonucleotide array (I) comprising at least

XX CC 25 different addresses (adapter sequences) with each comprising a

XX CC different capture probe selected from a group consisting of the sequences

XX CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target

XX CC nucleic acid sequence by attaching an adapter nucleic acid

XX CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target

XX CC nucleic acid and contacting the modified target nucleic acid with (I).

XX CC The steps of above method is useful for detecting a target nucleic acid,

XX CC which further comprises detecting the presence of the modified target

Query Match: 64.71% Indels: 0
 DB: 24 Gaps: 0

US-10-023-182-5 (1-9) x ABQ07160 (1-24)

OY 4 MetTripleThgInCys 9

DB 23 ATGTGATCAGCAGCTGC 6

RESULT 7

AAV50351/c

XX ID AAV50351 standard; cDNA; 19 BP.

XX AC AAV50351;

XX DT 27-OCT-1998 (first entry)

XX DE Human LAGE-1 PCR primer BLB56.

XX KM Human; LAGE-1; tumour associated protein; IL-1; diagnosis; tumour;

XX KM PCR primer; ss.

XX OS Synthetic.

XX FN WO9832855-A1.

XX PD 30-JUL-1998.

XX PF 27-JUN-1998; 98WO-US01445.

XX PR 27-JUN-1997; 97US-0791495.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Boon-Falleur T, De Smet C, Godelaine D, Lethe B.

XX PI Lucas S;

XX DR WPI; 1998-427951/36.

XX PT New isolated LAGE-1 tumour associated nucleic acids - used to

XX PT develop products for the diagnosis and treatment of LAGE-1

XX PT associated disorders, particularly tumours

XX PS Example 1; Page 50; 73pp; English.

XX CC The present sequence represents a PCR primer for LAGE-1 tumour

XX CC associated protein (TAP). The present invention also describes: (1) a

XX CC method for treating a subject with a disorder characterised by

XX CC expression of a LAGE-1 nucleic acid molecule or an expression product,

XX CC comprising administering to the subject autologous cytolytic T cells to

XX CC ameliorate the disorder, where the cytolytic T cells are specific for

XX CC complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic

XX CC fragment; (2) a method for treating a subject with a disorder

XX CC characterised by expression of a LAGE-1 nucleic acid molecule or an

XX CC expression product, comprising administering a LAGE-1 TAP or an

XX CC immunogenic fragment to ameliorate the disorder; and (3) a method for

XX CC selectively enriching a population of T cells with cytolytic T cells

XX CC specific for a LAGE-1 TAP comprising contacting an isolated population

Query Match: 64.71% Indels: 0
 DB: 24 Gaps: 0

US-10-023-182-5 (1-9) x ABQ07160 (1-24)

OY 4 MetTripleThgInCys 9

DB 23 ATGTGATCAGCAGCTGC 6

RESULT 7

AAV50351/c

XX ID AAV50351 standard; cDNA; 19 BP.

XX AC AAV50351;

XX DT 27-OCT-1998 (first entry)

XX DE Human LAGE-1 PCR primer BLB56.

XX KM Human; LAGE-1; tumour associated protein; IL-1; diagnosis; tumour;

XX KM PCR primer; ss.

XX OS Synthetic.

XX FN WO9832855-A1.

XX PD 30-JUL-1998.

XX PF 27-JUN-1998; 98WO-US01445.

XX PR 27-JUN-1997; 97US-0791495.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Boon-Falleur T, De Smet C, Godelaine D, Lethe B.

XX PI Lucas S;

XX DR WPI; 1998-427951/36.

XX PT New isolated LAGE-1 tumour associated nucleic acids - used to

XX PT develop products for the diagnosis and treatment of LAGE-1

XX PT associated disorders, particularly tumours

XX PS Example 1; Page 50; 73pp; English.

XX CC The present sequence represents a PCR primer for LAGE-1 tumour

XX CC associated protein (TAP). The present invention also describes: (1) a

XX CC method for treating a subject with a disorder characterised by

XX CC expression of a LAGE-1 nucleic acid molecule or an expression product,

XX CC comprising administering to the subject autologous cytolytic T cells to

XX CC ameliorate the disorder, where the cytolytic T cells are specific for

XX CC complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic

XX CC fragment; (2) a method for treating a subject with a disorder

XX CC characterised by expression of a LAGE-1 nucleic acid molecule or an

XX CC expression product, comprising administering a LAGE-1 TAP or an

XX CC immunogenic fragment to ameliorate the disorder; and (3) a method for

XX CC selectively enriching a population of T cells with cytolytic T cells

XX CC specific for a LAGE-1 TAP comprising contacting an isolated population

PN MO9954500-A2.
 XX 28-OCT-1999.
 PD 21-APR-1999; 99WO-IB00822.
 PF 21-APR-1998; 98US-0082614.
 XX 23-NOV-1998; 98US-0109732.
 PR (GSEST) GENSET.
 XX Cohen D, Blumenfeld M, Chumakov I;
 XX WPI; 2000-013267/01.
 DR Novel biallelic markers used to construct a high density disequilibrium
 XX map of the human genome -
 PT Claim 9, Page 1755; 2745pp; English.
 PS
 XX AA265654 to AA269578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AA269579 to AA277440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the
 CC invention have a variety of uses: they can be used for high density
 CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterisation of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other
 CC treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
 CC and 3367, are not actually given a sequence in the Sequence Listing
 CC from the present invention.
 XX
 SQ Sequence 21 BP; 7 A; 4 C; 3 G; 7 T; 0 other;
 Alignment Scores:
 Pred. No.: 377 Length: 21
 Score: 31.00 Matches: 5
 Percent Similarity: 71.43% Conservative: 0
 Best Local Similarity: 71.43% Mismatches: 2
 Query Match: 60.78% Indels: 0
 DB: 21 Gaps: 0
 US-10-023-182-5 (1-9) x AA272794 (1-21)
 QY 3 LeuMetTrpIleThrGlnCys 9
 DB 21 CTTGAATGATTTACAAATTGC 1
 RESULT 11
 AA2734559 standard; DNA; 29 BP.
 ID AA2734559;
 AC AA2734559;
 XX 11-SEP-1998 (first entry)
 DT Escherichia coli RNA 3'-terminal phosphate cyclase PCR primer.
 XX Escherichia coli RNA 3'-terminal cyclase; RNA synthesis; metabolism;
 XX PCR primer; RNA 3'-terminal cyclase; RNA synthesis; metabolism;
 KM study; mutagenic; ss.
 XX Synthetic.
 OS Escherichia coli.
 XX WO9745535-A1.
 PN 04-DEC-1997.
 PD
 XX

PF 20-MAY-1997; 97WO-EP02566.
 XX 24-MAY-1996; 96US-0018335.
 PR (NOVS) NOVARTIS AG.
 XX Filipowicz W, Genschik P;
 XX WPI; 1998-286352/25.
 DR New isolated RNA 3'-terminal phosphate cyclase nucleic acids - used
 PT to develop products for the study of RNA synthesis and metabolism in
 PT cells and for detection, diagnosis and therapy
 XX Example 2; Page 29; 71pp; English.
 PS
 XX The sequence is that a PCR primer which was used in the
 CC mutagenesis of RNA 3'-terminal phosphate cyclase.
 CC
 SQ Sequence 29 BP; 6 A; 10 C; 3 G; 10 T; 0 other;
 Alignment Scores:
 Pred. No.: 539 Length: 29
 Score: 31.00 Matches: 5
 Percent Similarity: 75.00% Conservative: 1
 Best Local Similarity: 62.50% Mismatches: 2
 Query Match: 60.78% Indels: 0
 DB: 19 Gaps: 0
 US-10-023-182-5 (1-9) x AA2734559 (1-29)
 QY 2 LeuMetTrpIleThrGlnCys 9
 DB 2 TTACATCTCGATCTTCAATGC 25
 RESULT 12
 AA210401/c
 ID AA210401 standard; DNA; 30 BP.
 XX
 AC AA210401;
 XX 15-NOV-1999 (first entry)
 DT PCR primer used to amplify cDNA encoding a calpain protein.
 XX PCR primer used to amplify cDNA encoding a calpain protein.
 XX Calpain; retinal tissue; retinal disorder; retina; PCR primer; ss.
 XX Synthetic.
 OS Rattus sp.
 XX WO9945107-A1.
 XX 10-SEP-1999.
 PD 26-FEB-1999; 99WO-IP00903.
 PF 02-MAR-1998; 98JP-0049430.
 XX (SENP) SENTU PHARM CO LTD.
 XX Azuma M, Fukiage C;
 XX WPI; 1999-540843/45.
 DR New Calpain protein and DNA encoding it, useful in the treatment and
 PT diagnosis of retinal disorders
 PT Example 2; Page 56; 64pp; Japanese.
 PS
 XX PCR primers AA210401-02 were used to amplify cDNA encoding a calpain
 CC protein (designated R188), which is specifically expressed in retinal
 CC tissue. The protein and nucleic acids are used for the prevention,
 CC treatment, diagnosis and investigation of retinal disorders.

```

XX SQ Sequence 30 BP; 8 A; 8 C; 5 G; 9 T; 0 other;
Alignment Scores:
Pred. No.: 560 Length: 30
Score: 31.00 Matches: 4
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 60.78% Indels: 0
DB: 20 Gaps: 0
US-10-023-182-5 (1-9) x AA210401 (1-30)
Qy 4 MetTpiethrgInCys 9
Db 21 ATATGATPACTCGCTGC 4
RESULT 13
AAQ94508/c
ID AAQ94508 standard; DNA; 29 BP.
XX AC AAQ94508;
XX DT 17-JAN-1996 (first entry)
XX DE Human/murine chimeric Ab HEF-RVL-M21d-g kappa PCR primer M21M3A.
XX KW Human; murine; chimeric antibody; HEF-RVL-M21d-g kappa;
XX KM medulloblastoma; brain tumour; treatment; diagnosis;
XX KW PCR primer M21M3A; ss.
XX OS Synthetic.
XX PN W09514041-A1.
XX PD 26-MAY-1995.
XX PF 19-OCT-1994; 94MO-JP01763.
XX PR 19-NOV-1993; 93JP-0291078.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX PI Ohtomo T, Sato K, Tsuchiya M;
XX DR WPI; 1995-200347/26.
XX PT Reconstituted antibody against human medulloblastoma cells -
PT contains high proportion of human antibody origin and has low
PT antigenicity
XX PS Example 5; Page 70; 120pp; Japanese.
XX CC AAQ94507 and AAQ94508 are a primer pair for the PCR amplification of
CC AAQ94506, which encodes AAR7668 the human/murine chimeric antibody
CC HEF-RVL-M21d-g kappa. The antibody is reactive with human medullo-
CC blastoma (a brain tumour) cells. The chimeric antibody can be
CC used in the diagnosis and treatment of this disease.
XX SQ Sequence 29 BP; 7 A; 10 C; 6 G; 6 T; 0 other;
Alignment Scores:
Pred. No.: 815 Length: 29
Score: 30.00 Matches: 3
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 60.00% Mismatches: 0
Query Match: 58.82% Indels: 0
DB: 16 Gaps: 0
US-10-023-182-5 (1-9) x AAQ94508 (1-29)
Qy 5 TpiethrgInCys 9

```

```

Db 28 TGGGTGACAGAGTGT 14
RESULT 14
AAT38622/c
ID AAT38622 standard; DNA; 29 BP.
XX AC AAT38622;
XX DT 09-DEC-1996 (first entry)
XX DE Chimeric human/murine Mab ONS-M21 fragment PCR primer M21M3A.
XX KW Murine; human; myeloblastoma; chimaera; monoclonal antibody;
XX KM chimaera; single stranded Fv region; low human antigenicity;
XX KM diagnosis; treatment; cerebral tumour; reshaped; primer; PCR;
XX KM polymerase chain reaction; ss.
XX OS Synthetic.
XX PN JP08169900-A.
XX PD 02-JUL-1996.
XX PF 18-NOV-1994; 94JP-0285057.
XX PR 18-OCT-1994; 94JP-0252166.
XX PR 19-NOV-1993; 93JP-0291078.
XX PA (CHUS ) CHUGAI PHARM CO LTD.
XX DR WPI; 1996-358509/36.
XX PT Reshaped anti-human myeloblastoma cell human antibody - has low
PT human antigenicity, and is therefore useful for diagnosis and
PT treatment of cerebral tumours, e.g. myeloblastoma
XX PS Example 5; Page 27; 45pp; Japanese.
XX CC The present sequence is a primer for a fragment of the chimaeric
CC human/murine monoclonal antibody (Mab) ONS-M21 cDNA. The Mab was
CC prepd. by combining light and heavy variable region DNA, from a
CC murine anti-human myeloblastoma cell Mab, with human light and
CC heavy constant region sequences, respectively to produce chimaeric
CC human/murine light and heavy chain DNA mols.. A recombinant vector
CC for the expression of the heavy and light chain DNA mols. was
CC prepd., and used to transform a host cell. The host cell was then
CC cultured, and the expression prodts. of the heavy and light chain
CC DNA mols. sepd. and connected with a peptide linker to produce a
CC single stranded Fv region. The reshaped Fv region has low human
CC antigenicity, and is therefore expected to be useful as an agent
CC for the diagnosis and treatment of cerebral tumours,
CC e.g. myeloblastoma.
XX SQ Sequence 29 BP; 7 A; 10 C; 6 G; 6 T; 0 other;
Alignment Scores:
Pred. No.: 815 Length: 29
Score: 30.00 Matches: 3
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 60.00% Mismatches: 0
Query Match: 58.82% Indels: 0
DB: 17 Gaps: 0
US-10-023-182-5 (1-9) x AAT38622 (1-29)
Qy 5 TpiethrgInCys 9
Db 28 TGGGTGACAGAGTGT 14
RESULT 15
AAF73764/c
ID AAF73764 standard; DNA; 31 BP.
XX

```



```

AC  AAF73764;
XX
DT  30-APR-2001 (first entry)
XX
DE  Probe for human SHP-2 DNA SEQ ID 4.
XX
XX  Antisense oligonucleotide; human, SHP-2; tyrosine phosphatase;
KM  phosphotyrosine; diabetes; inflammatory disease; tumour; inhibitor;
KW  probe; ss.
XX
XX  Homo sapiens.
XX
XX  W0200107655-A1.
XX
XX  01-FEB-2001.
XX
XX  19-JUL-2000; 2000MO-US19622.
XX
XX  21-JUL-1999; 99US-0358683.
XX
XX  (ISIS-) ISIS PHARM INC.
XX
XX  Bennett CF, Cowbert LM;
XX
XX  WPI; 2001-168572/17.
XX
XX  Novel antisense compound targeted to a nucleic acid molecule encoding
PT  human SHP-2 is useful for inhibiting the expression of human SHP-2 and
PT  treating diabetes and inflammatory disorders -
XX
XX  Example 13; Page 88; 98pp; English.
XX
XX  This invention relates to antisense oligonucleotide sequences which
CC  target DNA encoding human SHP-2 (a member of the family of non-membrane
CC  tyrosine phosphatases). Sequences AAF73768 - AAF73807 represent antisense
CC  oligonucleotides which have phosphotyrosine backbones, and optionally
CC  flanked with 5 base wings with 2'-methoxyethyl (MOE) nucleotides. These
CC  oligonucleotides target SHP-2 (represented in AAF73761) and inhibit its
CC  expression. Sequences AAF73762 - AAF73767 represent PCR primers and
CC  probes for human SHP-2 and GAPDH (glyceraldehyde 3-phosphate
CC  dehydrogenase) which are used in quantitative PCR analysis of SHP-2 mRNA
CC  levels. The antisense oligonucleotides are useful for inhibiting the
CC  expression of SHP-2 in human cells or tissues. The oligonucleotides are
CC  also useful for treating a human having a disease or condition associated
CC  with SHP-2 such as diabetes or an inflammatory disorder. The antisense
CC  compounds can be utilized for diagnostics, therapeutics, prophylaxis and
CC  as research reagents and kits. The antisense compounds may also be useful
CC  prophylactically, e.g. to prevent or delay infection, inflammation or
CC  tumour formation. The antisense compounds are useful for research and
CC  diagnostics.
XX
XX  SQ Sequence 31 BP; 10 A; 10 C; 5 G; 6 T; 0 other;
XX
XX  Alignment Scores:
XX  Pred. No.: 877
XX  Score: 30.00
XX  Percent Similarity: 100.00%
XX  Best Local Similarity: 66.67%
XX  Query Match: 58.82%
XX  DB: 22
XX
XX  US-10-023-182-5 (1-9) x AAF73764 (1-31)
XX
OY  2 LeuLeuMetThrIleThr 7
   ::::|||||:::
Db  19 AtcTgAtGtGgGtGACA 2

```

Search completed: February 21, 2004, 19:51:58
 Job time : 172 secs

Mon Feb 23 07:48:06 2004

us-10-023-182-5.rn1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2004, 19:28:16 ; Search time 39.4138 Seconds
(without alignments)
100.788 Million cell updates/sec

Title: US-10-023-182-5

Perfect score: 51

Sequence: 1 SLIMWTC 9

Scoring table: BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Fgapop 10.0 , Fgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 583842

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+; p2n.model -DBY=rlh
-Q=/cgn2_1/USFTO.spool/US10023182/rnucat_20022004_111043_21349/app.query.fasta_1.597
-DB=issued; Patents NA -OPM=faaap -SUFFIX=tni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blom62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=33
-USRR=US10023182 @cgn 1.1 95 @runat 20022004 111043 21349 -NCPU=6 -ICPU=3
-NO MMAR -LARGESQTRY -NEG_SCORES=0 -NAIT -DSBLOC=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: issued Patents NA:*
2: /cgn2_6/ptcdat/1/ina/5A COMB.seq:*
3: /cgn2_6/ptcdat/1/ina/5B COMB.seq:*
4: /cgn2_6/ptcdat/1/ina/6A COMB.seq:*
5: /cgn2_6/ptcdat/1/ina/6B COMB.seq:*
6: /cgn2_6/ptcdat/1/ina/PCFUS COMB.seq:*
7: /cgn2_6/ptcdat/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	62.7	19	1	US-08-791-495-3 Sequence 3, Appli
2	60.8	31	1	US-09-423-978-7150 Sequence 7150, Ap
3	60.8	31	4	US-09-622-880B-7 Sequence 7, Appli
4	60.8	30	4	US-08-646-285A-55 Sequence 35, Appli
5	58.8	31	3	US-09-358-683-4 Sequence 4, Appli
6	56.9	22	4	US-09-435-327A-7 Sequence 5, Appli
7	56.9	24	1	US-08-746-797-5 Sequence 5, Appli
8	56.9	24	1	US-08-927-387-5 Sequence 5, Appli
9	56.9	24	2	US-08-918-058-5 Sequence 5, Appli
10	54.9	18	1	US-08-284-860A-5 Sequence 5, Appli
11	54.9	18	1	US-08-318-867A-3 Sequence 3, Appli
12	54.9	18	3	US-08-430-277A-3 Sequence 3, Appli

13	54.9	20	2	US-08-775-009-9 Sequence 9, Appli
14	54.9	20	3	US-09-358-683-22 Sequence 22, Appli
15	54.9	20	3	US-09-489-868A-74 Sequence 74, Appli
16	54.9	26	4	US-09-142-481-5 Sequence 5, Appli
17	54.9	27	2	US-09-122-230-13 Sequence 13, Appli
18	54.9	27	3	US-08-893-654B-12 Sequence 12, Appli
19	54.9	28	3	US-08-348-548-24 Sequence 24, Appli
20	54.9	28	5	PCT-US95-15716-24 Sequence 24, Appli
21	54.9	30	3	US-09-033-055A-9 Sequence 9, Appli
22	54.9	31	1	US-07-975-526-15 Sequence 15, Appli
23	54.9	31	4	US-09-462-917A-141 Sequence 141, App
24	54.9	18	1	US-08-763-502-2 Sequence 2, Appli
25	52.9	20	1	US-08-317-450B-6 Sequence 6, Appli
26	52.9	20	3	US-08-800-593-6 Sequence 6, Appli
27	52.9	20	4	US-09-721-822A-77 Sequence 77, Appli
28	52.9	20	4	US-09-780-135-147 Sequence 147, App
29	52.9	21	3	US-08-952-376-4 Sequence 4, Appli
30	52.9	21	4	US-09-422-978-11318 Sequence 11318, A
31	52.9	23	4	US-09-306-420C-7 Sequence 7, Appli
32	52.9	24	3	US-09-481-288-6 Sequence 6, Appli
33	52.9	24	3	US-08-853-774-14 Sequence 14, Appli
34	52.9	27	1	US-08-038-932B-5 Sequence 5, Appli
35	52.9	30	3	US-08-836-561-105 Sequence 105, App
36	52.9	30	4	US-08-833-167-7 Sequence 7, Appli
37	52.9	32	4	US-09-344-837A-7 Sequence 7, Appli
38	52.9	32	4	US-07-658-908A-2 Sequence 2, Appli
39	52.9	33	1	US-06-463-224-61 Sequence 61, Appli
40	52.9	33	1	US-08-463-377-61 Sequence 61, Appli
41	52.9	33	6	5519127-18 Patent No. 5519127
42	51.0	18	2	US-08-844-550-1 Sequence 1, Appli
43	51.0	18	4	US-09-723-535-47 Sequence 47, Appli
44	51.0	26	6	US-08-821-984-1 Sequence 1, Appli
45	51.0	20	3	

ALIGNMENTS

RESULT 1
US-08-791-495-3/c
; Sequence 3, Application US/08791495
; Patent No. 5811519
GENERAL INFORMATION:
APPLICANT: Iech, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: IL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 10461/7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 19 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: YES
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-08-791-495-3

Alignment Scores:
 Pred. No.: 43.8 Length: 19
 Score: 32.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 62.75% Indels: 0
 DB: 1 Gaps: 0

US-10-023-182-5 (1-9) x US-08-791-495-3 (1-19)

Oy 1 SerLeuMetTyrIle 6
 Db 18 TCCCTGTGATGATGATC 1

RESULT 2
 US-09-422-978-7150/c
 Sequence 7150, Application US/09422978
 Patent No. 6537751

GENERAL INFORMATION:
 APPLICANT: Cohen, Daniel
 APPLICANT: Blumenfeld, Marra
 APPLICANT: Chumakov, Ilya
 TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
 FILE REFERENCE: GENEST.020CPI
 CURRENT APPLICATION NUMBER: US/09/422,978
 EARLIER FILING DATE: 1999-10-20
 EARLIER APPLICATION NUMBER: US 09/298,850
 EARLIER FILING DATE: 1999-04-21
 EARLIER APPLICATION NUMBER: US 60/109,732
 EARLIER FILING DATE: 1998-11-23
 EARLIER APPLICATION NUMBER: US 60/082,614
 EARLIER FILING DATE: 1998-04-21
 NUMBER OF SEQ ID NOS: 11796
 SEQ ID NO 7150
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Homo Sapiens
 FEATURE:
 NAME/KEY: primer_bind
 LOCATION: 1..21
 OTHER INFORMATION: upstream amplification primer 99-24936 for SEQ 3216,
 US-09-422-978-7150

Alignment Scores:
 Pred. No.: 74.3 Length: 21
 Score: 31.00 Matches: 5
 Percent Similarity: 71.43% Conservative: 0
 Best Local Similarity: 71.43% Mismatches: 2
 Query Match: 60.78% Indels: 0
 DB: 4 Gaps: 0

US-10-023-182-5 (1-9) x US-09-422-978-7150 (1-21)

Oy 3 LeuMetTyrIleThrGlnCys 9
 Db 21 CTGATGATGATTCACAAATTC 1

RESULT 3
 US-09-622-880B-7/c
 Sequence 7, Application US/09622880B
 Patent No. 6582932

GENERAL INFORMATION:
 APPLICANT: FUKIAGE, Chino
 APPLICANT: AZUMA, Mitsuyoshi
 TITLE OF INVENTION: NOVEL CALPIN AND DNA ENCODING THE SAME
 FILE REFERENCE: 2000-1125A/WMC/00177
 CURRENT APPLICATION NUMBER: US/09/622,880B
 CURRENT FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: JP 10-049430
 PRIOR FILING DATE: 1998-03-02
 NUMBER OF SEQ ID NOS: 16
 SEQ ID NO 7
 LENGTH: 30
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: primer
 US-09-622-880B-7

Alignment Scores:
 Pred. No.: 110 Length: 30
 Score: 31.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 66.67% Mismatches: 0
 Query Match: 60.78% Indels: 0
 DB: 4 Gaps: 0

US-10-023-182-5 (1-9) x US-09-622-880B-7 (1-30)

Oy 4 MetTyrIleThrGlnCys 9
 Db 21 ATATGATGATGATGATC 4

RESULT 4
 US-08-646-265A-55/c
 Sequence 55, Application US/08646265A
 Patent No. 6214973

GENERAL INFORMATION:
 APPLICANT: OHTOMO, Toshiniko
 APPLICANT: SATO, Koh
 APPLICANT: TSUCHIYA, Masayuki
 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
 TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
 NUMBER OF SEQUENCES: 132
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,265A
 FILING DATE: 09-SEP-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/JP94/01763
 FILING DATE: 19-OCT-1994
 PRIOR APPLICATION DATA: JP 5-291078
 FILING DATE: 19-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: WEGNER, Harold C.
 REGISTRATION NUMBER: 25,258
 REFERENCE/DOCKET NUMBER: 53466/184
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136

```
/ INFORMATION FOR SEQ ID NO: 55:
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 29 base pairs
/     TYPE: nucleic acid
/     STRANDEDNESS: single
/     TOPOLOGY: linear
/ US-08-646-265A-55
/
/ Alignment Scores:
/   Pred. No.:      161
/   Score:          30.00
/   Percent Similarity: 100.00%
/   Best Local Similarity: 60.00%
/   Query Match:    58.82%
/   DB:              3
/
/ US-10-023-182-5 (1-9) x US-08-646-265A-55 (1-29)
/
/ QY      5 TTTTleThrgInCys 9
/         |||::|||::|||
/ Db      28 TGGGTGACAGAGTGT 14
/
/ RESULT 5
/ US-09-358-683-4/c
/   Sequence 4, Application US/09358683
/   Patent No. 6200807
/   GENERAL INFORMATION:
/     APPLICANT: C. Frank Bennett
/     APPLICANT: Lex M. Cowsett
/     TITLE OF INVENTION: ANTISENSE MODULATION OF SHP-2 EXPRESSION
/     FILE REFERENCE: RTS-0082
/     CURRENT APPLICATION NUMBER: US/09/358,683
/     CURRENT FILING DATE: 1999-07-21
/     NUMBER OF SEQ ID NOS: 47
/     SEQ ID NO 4
/     LENGTH: 31
/     TYPE: DNA
/     ORGANISM: Artificial Sequence
/     FEATURE:
/     OTHER INFORMATION: PCR Probe
/ US-09-358-683-4
/
/ Alignment Scores:
/   Pred. No.:      173
/   Score:          30.00
/   Percent Similarity: 100.00%
/   Best Local Similarity: 66.67%
/   Query Match:    58.82%
/   DB:              3
/
/ US-10-023-182-5 (1-9) x US-09-358-683-4 (1-31)
/
/ QY      2 leuLeuMeetRpleThr 7
/         ::|||::|||::|||
/ Db      19 ATCTTGATGGGTGACA 2
/
/ RESULT 6
/ US-09-435-327A-7/c
/   Sequence 7, Application US/09435327A
/   Patent No. 6537766
/   GENERAL INFORMATION:
/     APPLICANT: Uckun, Patih M.
/     APPLICANT: Crotty, Mya L.
/     TITLE OF INVENTION: IKAROS ISOFORMS AND MUTANTS
/     FILE REFERENCE: 12152.35US01
/     CURRENT APPLICATION NUMBER: US/09/435,327A
/     CURRENT FILING DATE: 1999-11-05
/     PRIOR APPLICATION NUMBER: 60/107,229
/     PRIOR FILING DATE: 1998-11-05
/     NUMBER OF SEQ ID NOS: 27
/     SOFTWARE: PatentIn Ver. 2.1
/     SEQ ID NO 7
/     LENGTH: 22
```

```
/   TYPE: DNA
/   ORGANISM: Homo sapiens
/ US-09-435-327A-7
/
/ Alignment Scores:
/   Pred. No.:      181
/   Score:          29.00
/   Percent Similarity: 80.00%
/   Best Local Similarity: 80.00%
/   Query Match:    56.86%
/   DB:              4
/
/ US-10-023-182-5 (1-9) x US-09-435-327A-7 (1-22)
/
/ QY      5 TTTTleThrgInCys 9
/         |||::|||::|||
/ Db      20 TGGATCAGTCATGT 6
/
/ RESULT 7
/ US-08-746-797-5/c
/   Sequence 5, Application US/08746797
/   Patent No. 5759832
/   GENERAL INFORMATION:
/     APPLICANT: Gentry, Daniel
/     APPLICANT: Lonsdale, John
/     APPLICANT: Payne, David
/     APPLICANT: Pearson, Stewart
/     TITLE OF INVENTION: NOVEL FADH
/     NUMBER OF SEQUENCES: 7
/     CORRESPONDENCE ADDRESS:
/     ADDRESSEE: SmithKline Beecham Corporation
/     STREET: 709 Swedeland Road
/     CITY: King of Prussia
/     STATE: PA
/     COUNTRY: U.S.A.
/     ZIP: 19406-0939
/     COMPUTER READABLE FORM:
/     MEDIUM TYPE: Diskette
/     COMPUTER: IBM Compatible
/     OPERATING SYSTEM: DOS
/     SOFTWARE: FastSeq Version 1.5
/     CURRENT APPLICATION DATA:
/     APPLICATION NUMBER: US/08/746,797
/     FILING DATE:
/     CLASSIFICATION:
/     PRIOR APPLICATION DATA:
/     APPLICATION NUMBER: No. 5759832 Yet Assigned
/     FILING DATE: 23-OCT-1996
/     ATTORNEY/AGENT INFORMATION:
/     NAME: Gimm, Edward R
/     REGISTRATION NUMBER: 38,891
/     REFERENCE/DOCKET NUMBER: P50573
/     TELECOMMUNICATION INFORMATION:
/     TELEPHONE: 610-270-4478
/     TELEFAX: 610-270-5090
/     TELEX:
/
/ INFORMATION FOR SEQ ID NO: 5:
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 24 base pairs
/     TYPE: nucleic acid
/     STRANDEDNESS: single
/     TOPOLOGY: linear
/     MOLECULAR TYPE: Genomic DNA
/     HYPOTHETICAL: NO
/     ANTI-SENSE: NO
/     FRAGMENT TYPE:
/     ORIGINAL SOURCE:
/ US-08-746-797-5
/
/ Alignment Scores:
/   Pred. No.:      199
/   Score:          29.00
/   Percent Similarity: 75.00%
/
/ Length: 24
/ Matches: 4
/ Conservative: 2
```

Best Local Similarity: 50.00% Mismatches: 2
Query Match: 56.86% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-5 (1-9) x US-08-746-797-5 (1-24)

QY 2 LeuLeuMetTPrIleThrGlnCys 9
DB 24 GTAATCATGTGTGTAACACATTGT 1

RESULT 8

US-08-927-387-5/c
Sequence 5, Application US/08927387
Patent No. 5783432
GENERAL INFORMATION:
APPLICANT: Gentry, Daniel
APPLICANT: Lonsdale, John
APPLICANT: Payne, David
APPLICANT: Pearson, Stewart
TITLE OF INVENTION: NOVEL FABH
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,387
FILING DATE: 25-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/746,797
FILING DATE: 23-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50573
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-927-387-5

Alignment Scores:

Pred. No.: 199 Length: 24
Score: 29.00 Matches: 4
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 56.86% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-5 (1-9) x US-08-927-387-5 (1-24)

QY 2 LeuLeuMetTPrIleThrGlnCys 9
DB 24 GTAATCATGTGTGTAACACATTGT 1

DB 24 GTAATCATGTGTGTAACACATTGT 1

RESULT 9

US-08-918-058-5/c
Sequence 5, Application US/08918058
Patent No. 5885572
GENERAL INFORMATION:
APPLICANT: Gentry, Daniel
APPLICANT: Lonsdale, John
APPLICANT: Payne, David
APPLICANT: Pearson, Stewart
TITLE OF INVENTION: NOVEL FABH
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,058
FILING DATE: 25-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/746,797
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50573
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-918-058-5

Alignment Scores:

Pred. No.: 199 Length: 24
Score: 29.00 Matches: 4
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 56.86% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-5 (1-9) x US-08-918-058-5 (1-24)

QY 2 LeuLeuMetTPrIleThrGlnCys 9
DB 24 GTAATCATGTGTGTAACACATTGT 1

RESULT 10

US-08-284-860A-5/c
Sequence 5, Application US/08284860A
Patent No. 5643762
GENERAL INFORMATION:
APPLICANT: Ohshima, Atsushi

APPLICANT: Inouye, Sumiko
APPLICANT: Inouye, Masayori
TITLE OF INVENTION: METHOD FOR SYNTHESIZING SINGLE-STRANDED
TITLE OF INVENTION: STEM-LOOP DNAs, THE PRODUCTS AND USES THEREFOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates, P.C.
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,860A
FILING DATE: 02-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377.5577P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
TELEX: 834809
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-284-860A-5
Alignment Scores:
Pred. No.: 220
Score: 28.00
Percent Similarity: 100.00%
Best Local Similarity: 66.67%
Query Match: 54.90%
DB: 1
Gaps: 0
US-10-023-182-5 (1-9) x US-08-284-860A-5 (1-18)
QY 2 LeuLeuMeTTrpIleThr 7
|||:|||||
Db 18 CTGATCTGTGTGATTAACC 1
RESULT 11
US-08-318-867A-3/C
Sequence 3, Application US/08318867A
Patent No. 5714323
GENERAL INFORMATION:
APPLICANT: ATUSHI OHSHIMA
APPLICANT: MASAYORI INOUE
TITLE OF INVENTION: OVER EXPRESSION OF SINGLE-STRANDED
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES, P.C.
STREET: 230 S. 15th ST.
CITY: PHILADELPHIA, PA
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,867A
FILING DATE: MAY 4, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GERARD J. WEISER
REFERENCE/DOCKET NUMBER: 377.6120P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 875-8383
TELEFAX: (215) 875-8394
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-318-867A-3
Alignment Scores:
Pred. No.: 220
Score: 28.00
Percent Similarity: 100.00%
Best Local Similarity: 66.67%
Query Match: 54.90%
DB: 1
Gaps: 0
US-10-023-182-5 (1-9) x US-08-318-867A-3 (1-18)
QY 2 LeuLeuMeTTrpIleThr 7
|||:|||||
Db 18 CTGATCTGTGTGATTAACC 1
RESULT 12
US-08-430-277A-3/C
Sequence 3, Application US/08430277A
Patent No. 6043028
GENERAL INFORMATION:
APPLICANT: Ohshima, Atushi
APPLICANT: Inouye, Masayori
APPLICANT: Inouye, Sumiko
TITLE OF INVENTION: METHOD FOR SYNTHESIZING SINGLE-STRANDED
TITLE OF INVENTION: STEM-LOOP DNAs, THE PRODUCTS AND USES THEREFORE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,277A
FILING DATE: 28-APR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REFERENCE/DOCKET NUMBER: 913(377).5820
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-430-277A-3

Alignment Scores: 220 Length: 18
Pred. No.: 28.00 Matches: 4
Score: 28.00
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 54.90% Indels: 0
DB: 3 Gaps: 0

US-10-023-182-5 (1-9) x US-08-430-277A-3 (1-18)

QY 2 LeuMetTPIleThr 7
18 CTGATCTGTGATTAACC 1

RESULT 13
US-08-775-009-9

Sequence 9, Application US/08775009
Patent No. 5935783
GENERAL INFORMATION:
APPLICANT: Gong, Weilong
APPLICANT: Emanuel, Beverly S.
APPLICANT: Budarf, Marcia L.
APPLICANT: Roe, Bruce
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digestion and
TITLE OF INVENTION: Velloicardiofacial Syndrome Minimal Critical Region
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5935783ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Tjuillio, Doreen Yalco
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-775-009-9

Alignment Scores:

Pred. No.: 247 Length: 20
Score: 28.00 Matches: 4
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 80.00% Mismatches: 0
Query Match: 54.90% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-5 (1-9) x US-08-775-009-9 (1-20)

QY 3 LeuMetTPIleThr 7

DB 5 CTGATGTGGGTAAACA 19

RESULT 14
US-09-358-683-22
Sequence 22, Application US/09358683
Patent No. 6200807
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF SHP-2 EXPRESSION
FILE REFERENCE: RTS-0082
CURRENT APPLICATION NUMBER: US/09/358,683
CURRENT FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 22
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-358-683-22

Alignment Scores: 247 Length: 20
Pred. No.: 28.00 Matches: 4
Score: 28.00
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 80.00% Mismatches: 0
Query Match: 54.90% Indels: 0
DB: 3 Gaps: 0

US-10-023-182-5 (1-9) x US-09-358-683-22 (1-20)

QY 3 LeuMetTPIleThr 7
1 TTGATGTGGGTGACA 15

RESULT 15
US-09-489-868A-74
Sequence 74, Application US/09489868A
Patent No. 6265216
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyat
TITLE OF INVENTION: ANTISENSE MODULATION OF COT ONCOGENE EXPRESSION
FILE REFERENCE: RTS-0113
CURRENT APPLICATION NUMBER: US/09/489,868A
CURRENT FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 74
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-489-868A-74

Alignment Scores: 247 Length: 20
Pred. No.: 28.00 Matches: 4
Score: 28.00
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 54.90% Indels: 0
DB: 3 Gaps: 0

US-10-023-182-5 (1-9) x US-09-489-868A-74 (1-20)

QY 3 LeuMetTPIleThrIn 8
1 ATATGTGGTTACACAG 18

Search completed: February 21, 2004, 22:53:54
Job time : 40.4138 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: February 21, 2004, 21:41:37 ; Search time 216.331 Seconds
(without alignments)
152.826 Million cell updates/sec

Title: US-10-023-182-5
Perfect score: 51
Sequence: 1 SLIMWITQC 9

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 1147742

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=X1h
-O=/cgn2_1/USPTO.spool/US10023182/runac_20022004_111045_21435/app.query.fasta_1.597
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rmdb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdd -LIST=45 -DOCALLIGN=200 -THR SCORE=Pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=33 -USER=US10023182@cgn2_1.1.560@runac_20022004_111045_21435 -NCPU=6
-ICPU=3 -NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMECUT=120 -MAIN_TIMECUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/prodata/1/pubna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubna/US07_PUBCOMB.seq:*
3: /cgn2_6/prodata/1/pubna/US06_PUBCOMB.seq:*
4: /cgn2_6/prodata/1/pubna/US06_PUBCOMB.seq:*
5: /cgn2_6/prodata/1/pubna/US07_PUBCOMB.seq:*
6: /cgn2_6/prodata/1/pubna/US07_PUBCOMB.seq:*
7: /cgn2_6/prodata/1/pubna/US08_PUBCOMB.seq:*
8: /cgn2_6/prodata/1/pubna/US08_PUBCOMB.seq:*
9: /cgn2_6/prodata/1/pubna/US09_PUBCOMB.seq:*
10: /cgn2_6/prodata/1/pubna/US09_PUBCOMB.seq:*
11: /cgn2_6/prodata/1/pubna/US09_PUBCOMB.seq:*
12: /cgn2_6/prodata/1/pubna/US09_PUBCOMB.seq:*
13: /cgn2_6/prodata/1/pubna/US09_PUBCOMB.seq:*
14: /cgn2_6/prodata/1/pubna/US10_PUBCOMB.seq:*
15: /cgn2_6/prodata/1/pubna/US10_PUBCOMB.seq:*
16: /cgn2_6/prodata/1/pubna/US10_PUBCOMB.seq:*
17: /cgn2_6/prodata/1/pubna/US10_PUBCOMB.seq:*
18: /cgn2_6/prodata/1/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result Query *
No. Score Match Length DB ID Description

SUMMARIES

1	33	64.7	24	11	US-09-940-185-1601	Sequence 1601, Ap
2	33	64.7	25	15	US-10-098-2638-115637	Sequence 115637, Ap
3	33	64.7	25	15	US-10-098-2638-115638	Sequence 115638, Ap
4	31	60.8	20	15	US-10-222-334-23	Sequence 23, Appl
5	31	60.8	21	12	US-10-349-143-7150	Sequence 7150, Ap
6	30	58.8	25	15	US-10-098-2638-556835	Sequence 556835, A
7	30	58.8	25	15	US-10-098-2638-892921	Sequence 892921, A
8	30	58.8	25	15	US-10-098-2638-892922	Sequence 892922, A
9	30	58.8	29	11	US-09-749-873-55	Sequence 55, Appl
10	29	56.9	17	13	US-10-230-006-763	Sequence 763, App
11	29	56.9	17	13	US-10-230-006-764	Sequence 764, App
12	29	56.9	22	12	US-10-395-011-7	Sequence 7, Appl
13	29	56.9	24	9	US-09-809-333-74	Sequence 74, Appl
14	29	56.9	25	15	US-10-098-2638-1045	Sequence 1045, Ap
15	29	56.9	25	15	US-10-098-2638-64527	Sequence 64527, A
16	29	56.9	25	15	US-10-098-2638-64528	Sequence 64528, A
17	29	56.9	26	11	US-09-910-185-5	Sequence 5, Appl
18	29	56.9	29	13	US-10-209-336-3	Sequence 3, Appl
19	29	56.9	31	11	US-09-740-332-7593	Sequence 7593, Ap
20	29	56.9	31	11	US-09-740-332-8186	Sequence 8186, Ap
21	29	56.9	31	13	US-09-817-879-7593	Sequence 7593, Ap
22	29	56.9	31	13	US-09-817-879-8186	Sequence 8186, Ap
23	28	54.9	20	11	US-09-860-8368-23	Sequence 23, Appl
24	28	54.9	21	12	US-10-136-728-105	Sequence 105, App
25	28	54.9	22	9	US-09-930-218-14	Sequence 14, Appl
26	28	54.9	22	13	US-10-431-438-14	Sequence 14, Appl
27	28	54.9	23	10	US-09-957-667-7	Sequence 7, Appl
28	28	54.9	23	10	US-10-060-301-15	Sequence 15, Appl
29	28	54.9	23	15	US-10-215-112-2584	Sequence 2584, Ap
30	28	54.9	25	15	US-10-098-2638-3751	Sequence 3751, Ap
31	28	54.9	25	15	US-10-098-2638-14341	Sequence 14341, A
32	28	54.9	25	15	US-10-098-2638-44679	Sequence 44679, A
33	28	54.9	25	15	US-10-098-2638-45503	Sequence 45503, A
34	28	54.9	25	15	US-10-098-2638-60841	Sequence 60841, A
35	28	54.9	26	12	US-09-930-512-81	Sequence 81, Appl
36	28	54.9	28	13	US-10-087-887-102	Sequence 102, Appl
37	28	54.9	29	13	US-10-181-157-18	Sequence 18, Appl
38	28	54.9	29	13	US-10-357-043-26	Sequence 26, Appl
39	28	54.9	31	11	US-09-740-332-5328	Sequence 5328, Ap
40	28	54.9	31	13	US-09-817-879-5328	Sequence 5328, Ap
41	28	54.9	33	9	US-09-878-484-6	Sequence 6, Appl
42	28	54.9	33	9	US-10-320-786-141	Sequence 141, App
43	28	54.9	33	13	US-09-756-071B-6	Sequence 6, Appl
44	27	52.9	20	9	US-09-909-320-327	Sequence 327, App
45	27	52.9	20	10	US-09-909-320-327	Sequence 327, App

ALIGNMENTS

RESULT 1
US-09-940-185-1601
; Sequence 1601, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1601
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-1601

```
Alignment Scores:
Pred. No.: 174 Length: 24
Score: 33.00 Matches: 5
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 64.71% Indels: 0
DB: 11 Gaps: 0

US-10-023-182-5 (1-9) x US-09-940-185-1601 (1-24)

QY 4 NetTPrleThrgInCys 9
DB 2 ATGGATCACCAGCTGC 19

RESULT 2
US-10-098-263B-115637
; Sequence 115637, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; CURRENT APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 115637
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-115637

Alignment Scores:
Pred. No.: 182 Length: 25
Score: 33.00 Matches: 4
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 80.00% Mismatches: 0
Query Match: 64.71% Indels: 0
DB: 15 Gaps: 0

US-10-023-182-5 (1-9) x US-10-098-263B-115637 (1-25)

QY 5 TrrpleThrgInCys 9
DB 8 TGGATCACCAGCTGT 22

RESULT 3
US-10-098-263B-115638
; Sequence 115638, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; CURRENT APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 115638
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-115638

Alignment Scores:
Pred. No.: 182 Length: 25
Score: 33.00 Matches: 4
Percent Similarity: 100.00% Conservative: 1
Query Match: 64.71% Indels: 0
DB: 15 Gaps: 0

US-10-023-182-5 (1-9) x US-10-022-334-23 (1-20)

QY 5 TrrpleThrgInCys 9
DB 15 TGGATCACCAGATGC 1

RESULT 5
US-10-349-143-7150/C
; Sequence 7150, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marra
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7150
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
```

```
FEATURE:
/ NAME/KEY: primer_bind
/ LOCATION: 1..21
/ OTHER INFORMATION: upstream amplification primer 99-24936 for SEQ 3216,
US-10-349-143-7150

Alignment Scores:
Pred. No.: 350          Length: 21
Score: 31.00           Matches: 5
Percent Similarity: 71.43%  Conservative: 0
Best Local Similarity: 71.43%  Mismatches: 2
Query Match: 60.78%         Indels: 0
DB: 12                  Gaps: 0

US-10-023-182-5 (1-9) x US-10-349-143-7150 (1-21)

QY 3 LeuMetTPrleThgInCys 9
Db 21 CTTGATCGATTACAAATTC 1

RESULT 6
US-10-098-263B-56835
/ Sequence 56835, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ PRIOR FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 56835
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-56835

Alignment Scores:
Pred. No.: 642          Length: 25
Score: 30.00           Matches: 3
Percent Similarity: 100.00%  Conservative: 2
Best Local Similarity: 60.00%  Mismatches: 0
Query Match: 58.82%         Indels: 0
DB: 15                  Gaps: 0

US-10-023-182-5 (1-9) x US-10-098-263B-56835 (1-25)

QY 5 TPrleThgInCys 9
Db 3 TGGCTAACGAGTGT 17

RESULT 7
US-10-098-263B-89291
/ Sequence 89291, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ PRIOR FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 89291
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-89291
```

```
Alignment Scores:
Pred. No.: 642          Length: 25
Score: 30.00           Matches: 5
Percent Similarity: 85.71%  Conservative: 1
Best Local Similarity: 71.43%  Mismatches: 1
Query Match: 58.82%         Indels: 0
DB: 15                  Gaps: 0

US-10-023-182-5 (1-9) x US-10-098-263B-89291 (1-25)

QY 1 SerLeuMetTPrleThr 7
Db 5 TCTCTCTCGAGTGGTTGACT 25

RESULT 8
US-10-098-263B-89292
/ Sequence 89292, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ PRIOR FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 89292
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-89292

Alignment Scores:
Pred. No.: 642          Length: 25
Score: 30.00           Matches: 5
Percent Similarity: 85.71%  Conservative: 1
Best Local Similarity: 71.43%  Mismatches: 1
Query Match: 58.82%         Indels: 0
DB: 15                  Gaps: 0

US-10-023-182-5 (1-9) x US-10-098-263B-89292 (1-25)

QY 1 SerLeuMetTPrleThr 7
Db 5 TCTCTCTCGAGTGGTTGACT 25

RESULT 9
US-09-749-873-55/c
/ Sequence 55, Application US/09749873
/ Publication No. US20030023045A1
/ GENERAL INFORMATION:
/ APPLICANT: OHTOMO, Toshihiko
/ SATO, Koh
/ TSUCHIYA, Masayuki
/ TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
/ MEDULLOBLASTOMA CELLS
/ NUMBER OF SEQUENCES: 132
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/09/749,873
FILING DATE: 29-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,265
FILING DATE: 1996-09-09
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-Nov-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-749-873-55

Alignment Scores:
Pred. No.: 753 Length: 29
Score: 30.00 Matches: 3
Percent Similarity: 100.00% Conservatve: 2
Best Local Similarity: 60.00% Mismatches: 0
Query Match: 58.82% Indels: 0
DB: 11 Gaps: 0

US-10-023-182-5 (1-9) x US-09-749-873-55 (1-29)

QY 5 TrrleThrgInCys 9
Db 28 TGGGTGACAGAGTGT 14

RESULT 10
US-10-230-006-763
Sequence 763, Application US/10230006
Publication No. US20030191077A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Fossnaugh, Kathy
TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI
FILE REFERENCE: 400/056 (MEH801-1110)
CURRENT APPLICATION NUMBER: US/10/230,006
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US 60/315,315
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 2678
SOFTWARE: PatentIn version 3.0
SEQ ID NO 763
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-230-006-763

Alignment Scores:
Pred. No.: 646 Length: 17
Score: 29.00 Matches: 4
Percent Similarity: 80.00% Conservatve: 1
Best Local Similarity: 80.00% Mismatches: 0
Query Match: 56.86% Indels: 0
DB: 13 Gaps: 0

US-10-023-182-5 (1-9) x US-10-230-006-763 (1-17)

QY 5 TrrleThrgInCys 9
Db 11 TrrleThrgInCys 9

Db 3 UGAGUCACUCUCUC 17

RESULT 11
US-10-230-006-764
Sequence 764, Application US/10230006
Publication No. US20030191077A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Fossnaugh, Kathy
TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI
FILE REFERENCE: 400/056 (MEH801-1110)
CURRENT APPLICATION NUMBER: US/10/230,006
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US 60/315,315
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 2678
SOFTWARE: PatentIn version 3.0
SEQ ID NO 764
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-230-006-764

Alignment Scores:
Pred. No.: 646 Length: 17
Score: 29.00 Matches: 4
Percent Similarity: 80.00% Conservatve: 1
Best Local Similarity: 80.00% Mismatches: 0
Query Match: 56.86% Indels: 0
DB: 13 Gaps: 0

US-10-023-182-5 (1-9) x US-10-230-006-764 (1-17)

QY 5 TrrleThrgInCys 9
Db 1 UGAGUCACUCUCUC 15

RESULT 12
US-10-395-011-7/c
Sequence 7, Application US/10395011
Publication No. US2004002096A1
GENERAL INFORMATION:
APPLICANT: Uckun, Farh M.
APPLICANT: Croty, Mya L.
TITLE OF INVENTION: IRAROS ISOFORMS AND MUTANTS
FILE REFERENCE: 12152.35USU1
CURRENT APPLICATION NUMBER: US/10/395,011
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 09/435,327
PRIOR FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 60/107,229
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens
US-10-395-011-7

Alignment Scores:
Pred. No.: 852 Length: 22
Score: 29.00 Matches: 4
Percent Similarity: 80.00% Conservatve: 1
Best Local Similarity: 80.00% Mismatches: 0
Query Match: 56.86% Indels: 0
DB: 12 Gaps: 0

US-10-023-182-5 (1-9) x US-10-395-011-7 (1-22)

QY 5 TrrleThrgInCys 9
Db 11 TrrleThrgInCys 9

```
DB      20 TGGATCAGCTCATGT 6
RESULT 13
US-09-809-323-74
; Sequence 74, Application US/09809323
; Patent No. US20020098487A1
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, Koji et al.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTING FUNGI
; FILE REFERENCE: 0760-0286P
; CURRENT APPLICATION NUMBER: US/09/809,323
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent version 3.1
; SEQ ID NO 74
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer targeted to Aspergillus terreus
US-09-809-323-74

Alignment Scores:
Pred. No.:      935      Length:      24
Score:          29.00     Matches:      4
Percent Similarity: 83.33% Conservaive: 1
Best Local Similarity: 66.67% Mismatches: 1
Query Match:    56.86%   Indels:      0
DB:             9       Gaps:        0

US-10-023-182-5 (1-9) x US-09-809-323-74 (1-24)
QY      4 MetTpIleThrGInCys 9
DB      2 TTATGGCAACCAATGC 19

RESULT 14
US-10-098-263B-1045/C
; Sequence 1045, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 1045
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-1045

Alignment Scores:
Pred. No.:      977      Length:      25
Score:          29.00     Matches:      4
Percent Similarity: 85.71% Conservaive: 2
Best Local Similarity: 57.14% Mismatches: 1
Query Match:    56.86%   Indels:      0
DB:             15      Gaps:        0

US-10-023-182-5 (1-9) x US-10-098-263B-1045 (1-25)
QY      1 SerLeuMetTyrIleThr 7
DB      22 AGTACTATCATGTGGGTAACG 2

RESULT 15
US-10-098-263B-64527/C
; Sequence 64527, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 64527
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-64527

Alignment Scores:
Pred. No.:      977      Length:      25
Score:          29.00     Matches:      4
Percent Similarity: 80.00% Conservaive: 0
Best Local Similarity: 80.00% Mismatches: 1
Query Match:    56.86%   Indels:      0
DB:             15      Gaps:        0

US-10-023-182-5 (1-9) x US-10-098-263B-64527 (1-25)
QY      5 TrpIleThrGInCys 9
DB      21 TGGATCAGCTCTTGT 7

Search completed: February 22, 2004, 00:58:47
Job time : 216.931 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2004, 19:17:36 / Search time 1303.14 Seconds

(without alignments)
167.857 Million cell updates/sec

SUMMARIES

29: gb_gss2.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Title: US-10-023-182-5
Perfect score: 51
Sequence: 1 SLMMWITQC 9
Scoring table: BIOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0
Searched: 22781392 segs, 1215238056 residues
Total number of hits satisfying chosen parameters: 43814
Minimum DB seq length: 0
Maximum DB seq length: 33
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xih
-O/cgmr2_1/USPFO.spool/US10023182/runat.20022004.111043.21331/app.query.fasta_1.597
-DB=CGMR2 -CGMT=fastap -SUFFIX=ret -MINMATCH=0.1 -LOOPC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biocum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=33
-USER=US10023182 @CGN 1.1 4382 @runat.20022004.111043.21331 -NCFU=6 -ICPU=3
-NO_MMAP -LARGESOURCY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

BST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estmy.*
6: em_estpl.*
7: em_estro.*
8: em_hlc.*
9: gb_est1.*
10: gb_est2.*
11: gb_hlc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vit.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pio.*
25: em_gss_rpd.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*

Result No. Score Query Match Length DB ID

Result No.	Score	Query Match Length DB ID	Description
1	28	54.9 32 9	AU006847
2	27	52.9 27 2	TA239F10P
3	27	52.9 31 28	AZ845348
4	27	52.9 32 12	BG762950
5	26	51.0 21 28	AZ660221
6	26	51.0 24 28	AZ954670
7	26	51.0 28 28	AZ811336
8	26	51.0 29 29	BZ765533
9	26	51.0 31 28	AZ969930
10	26	51.0 32 28	AZ785127
11	25	49.0 20 28	AZ478502
12	25	49.0 25 28	BH757571
13	25	49.0 28 9	AA466466
14	25	49.0 28 28	AZ475208
15	25	49.0 28 28	AZ610699
16	25	49.0 28 29	TA352E02Q
17	25	49.0 32 28	AZ303920
18	25	49.0 33 9	AV634299
19	24	47.1 20 28	AZ478502
20	24	47.1 22 28	AZ311475
21	24	47.1 22 28	AZ336549
22	24	47.1 24 28	AZ331582
23	24	47.1 24 28	AZ786547
24	24	47.1 28 9	A1667580
25	24	47.1 28 28	AZ436128
26	24	47.1 28 28	AZ595788
27	24	47.1 28 29	BZ286269
28	24	47.1 31 9	AA57129
29	24	47.1 31 28	AZ372016
30	24	47.1 32 28	AZ803519
31	24	47.1 33 14	D45809
32	24	47.1 33 14	D45809
33	24	47.1 33 28	AZ766467
34	24	47.1 33 28	AZ686781
35	23	45.1 21 28	AZ355490
36	23	45.1 22 28	AZ484950
37	23	45.1 24 29	TA20E11P
38	23	45.1 26 29	TA124A10Q
39	23	45.1 26 29	TA128F12P
40	23	45.1 30 28	BZ384708
41	23	45.1 30 28	AZ486857
42	23	45.1 31 9	A1379850
43	23	45.1 31 14	R52745
44	23	45.1 31 28	AZ955226
45	23	45.1 32 28	AZ407183

ALIGNMENTS

RESULT 1
AU006847
LOCUS
DEFINITION
AU006847 Schizosaccharomyces pombe 32 bp mRNA linear EST 31-JUL-1998
ACCESSION
AU006847
VERSION
AU006847.1 GI:3343305
KEYWORDS
EST.
SOURCE
Schizosaccharomyces pombe (fission yeast)
ORGANISM
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.

REFERENCE 1 (bases 1 to 32)
 AUTHORS Moritomo, M. and Mita, K.
 TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe
 JOURNAL Unpublished
 COMMENT Contact: Mitsunori Moritomo
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: moritomo@nirs.go.jp
 FEATURES Location/Qualifiers
 source 1..32
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc01028"
 /sex="h minus"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 12 a 3 c 3 g 14 t
 ORIGIN

Alignment Scores:
 Pred. No.: 7.81e+03 Length: 32
 Score: 28.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 66.67% Mismatches: 0
 Query Match: 54.90% Indels: 0
 DB: 9 Gaps: 0

US-10-023-182-5 (1-9) x AU006847 (1-32)

QY 2 LeuLeuMetTrrpIleThr 7
 Db 1.1 ATACTGTATGATTACCA 28

RESULT 2
 TA239F10F/c 27 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 239f10, forward sequence.
 DEFINITION
 genomic survey sequence.
 ACCESSION AL481728
 VERSION AL481728.1 GI:11847244
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 source 1..27
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="239f10"

BASE COUNT 10 a 7 c 5 g 5 t
 ORIGIN

Alignment Scores:
 Pred. No.: 8.98e+03 Length: 27
 Score: 27.00 Matches: 3
 Percent Similarity: 83.33% Conservative: 2
 Best Local Similarity: 50.00% Mismatches: 1
 Query Match: 52.94% Indels: 0
 DB: 29 Gaps: 0

US-10-023-182-5 (1-9) x TA239F10P (1-27)

QY 4 MetTrrpIleThrGlnCys 9
 Db 23 ATTTGGGTATCATGAT 6

RESULT 3
 AZ845348 31 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0145C07F Mouse 10kb plasmid UGCM library Mus musculus genomic
 DEFINITION
 clone UGCM2M0145C07 F, genomic survey sequence.
 ACCESSION AZ845348
 VERSION AZ845348.1 GI:13015256
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0145 row: C column: 07
 Seq primer: CGTTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 31.
 Location/Qualifiers
 source 1..31
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCM0145C07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCM library"
 /note="Vector: pMD22uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gll4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 11 a 5 c 7 g 8 t
ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	1.11e+04	31	4	4	0	0
Percent Similarity:	27.00		1	4		
Best Local Similarity:	55.56%					
Query Match:	44.44%					
DB:	52.94%					

US-10-023-182-5 (1-9) x AZ845348 (1-31)

QY 1 SerleuMetThrlleThrgInCy 9
Db 27 TCCATTAATTCGTGTTTACCAAGTC 1

RESULT 4

BG762950 32 bp mRNA linear EST 15-MAY-2001
LOCUS 602735196F1 NIH_MGC_49 Homo sapiens cDNA IMAGE:4860550 5',
DEFINITION mRNA sequence.

ACCESSION BG762950
VERSION BG762950.1 GI:14073603
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 32)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gqabps-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LICM1717 row: P column: 23
High quality sequence stop: 32.
Location/Qualifiers

FEATURES

source

1. 32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4860550"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_49"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory

of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	1.16e+04	32	4	0	0	0
Percent Similarity:	27.00		1	0		
Best Local Similarity:	80.00%					
Query Match:	80.00%					
DB:	52.94%					

US-10-023-182-5 (1-9) x BG762950 (1-32)

QY 5 TTPleThrgInCy 9
Db 3 TGGATCTTCAGTC 17

RESULT 5

AZ660221 21 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0538M09F Mouse 10kb plasmid U08C1M library Mus musculus genomic
DEFINITION clone U08C1M0538M09 F, genomic survey sequence.

ACCESSION AZ660221
VERSION AZ660221.1 GI:11979367
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0538 row: M column: 09
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES

source

1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0538M09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid U08C1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/shares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapored mouse DNA was annealed to adapored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

7 a 11 c 1 g 2 t

Alignment Scores:

Pred. No.: 9.12e+03 Length: 21
Score: 26.00 Matches: 3
Percent Similarity: 80.00% Conservatve: 1
Best Local Similarity: 60.00% Mismatches: 1
Query Match: 50.98% Indels: 0
DB: 28 Gaps: 0

US-10-023-182-5 (1-9) x AZ660221 (1-21)

Qy 5 TTP1lethrgInCys 9
17 TGGGTGGTCACTAGT 3

RESULT 6

AZ954670/c 24 bp DNA linear GSS 27-APR-2001

LOCUS 2M0220N20F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

DEFINITION clone UUGC2M0220N20 F, genomic survey sequence.

ACCESSION AZ954670

VERSION AZ954670.1 GI:13825897

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 24)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0220 row: N column: 20

Seq primer: CGTTGTAAACGACGCCACGT

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1. 24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0220N20"

/sex="female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapored mouse DNA was annealed to adapored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

9 a 1 c 4 g 10 t

Alignment Scores:

Pred. No.: 1.12e+04 Length: 24
Score: 26.00 Matches: 5
Percent Similarity: 75.50% Conservatve: 1
Best Local Similarity: 62.50% Mismatches: 2
Query Match: 50.98% Indels: 0
DB: 28 Gaps: 0

US-10-023-182-5 (1-9) x AZ954670 (1-24)

Qy 2 Leu1eMetrTTP1lethrgInCys 9

Db 24 ATTATAAATTAAATCAACCAATGT 1

RESULT 7

AZ811336 28 bp DNA linear GSS 20-FEB-2001

LOCUS 2M0077L18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION clone UUGC2M0077L18 F, genomic survey sequence.

ACCESSION AZ811336

VERSION AZ811336.1 GI:12979325

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 28)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0077 row: L column: 18

Seq primer: CGTTGTAAACGACGCCACGT

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

1. 28

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0077L18"

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 10 c 5 g 8 t

ORIGIN

Alignment Scores:

Pred. No.:	1.41e+04	Length:	28
Score:	26.00	Matches:	4
Percent Similarity:	66.67%	Conservative:	0
Best Local Similarity:	66.67%	Mismatches:	2
Query Match:	50.98%	Indels:	0
DB:	28	Gaps:	0

US-10-023-182-5 (1-9) x AZ811336 (1-28)

QY 4 MetTPIleThgInCys 9

Db 20 ATGTGTGAGTACATGC 3

RESULT 8 BZ765533 29 bp DNA linear GSS 13-MAR-2003

LOCUS SALK_131641.20.05 x Arabidopsis thaliana TDNA insertion lines

DEFINITION Arabidopsis thaliana genomic clone SALK_131641.20.05.x, genomic survey sequence.

ACCESSION BZ765533

VERSION BZ765533.1 GI:28938086

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J., and Ecker,J.R. A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished

JOURNAL Contact: Joseph R. Ecker

COMMENT The Salk Institute Genomic Analysis Laboratory (SIGAL)

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x11752

Fax: 858 558 6379

Email: ecker@salik.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At3g46620.

Class: TDNA tagged

Location/Qualifiers

1. 29

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_131641.20.05.x"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 4 a 6 c 6 g 13 t

ORIGIN

Alignment Scores:

Pred. No.:	1.49e+04	Length:	29
Score:	26.00	Matches:	5
Percent Similarity:	83.33%	Conservative:	0
Best Local Similarity:	83.33%	Mismatches:	1
Query Match:	50.98%	Indels:	0
DB:	29	Gaps:	0

US-10-023-182-5 (1-9) x BZ765533 (1-29)

QY 1 SerLeuMetTPIle 6

Db 5 TCATTACTCCCTTGATT 22

RESULT 9 AZ969930 31 bp DNA linear GSS 27-APR-2001

LOCUS 2M0242F24R Mouse 10kb plasmid UGCGM library Mus musculus genomic

DEFINITION clone UGCG2M0242F24 R, genomic survey sequence.

ACCESSION AZ969930

VERSION AZ969930.1 GI:13841157

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,F., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished

JOURNAL Contact: Robert B. Weiss

COMMENT University of Utah Genome Center

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0242 row: F column: 24

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 31.

Location/Qualifiers

1. 31

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG2M0242F24"

/sex="Female"

/lab host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCGM library"

/note="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 ligated DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 7 a 9 c 6 g 9 t

Alignment Scores:
 Pred. No.: 1.65e+04 Length: 31
 Score: 26.00 Matches: 3
 Percent Similarity: 71.43% Conservative: 2
 Best Local Similarity: 42.86% Mismatches: 0
 Query Match: 50.98% Indels: 0
 Gaps: 0

US-10-023-182-5 (1-9) x AZ969930 (1-31)

Qy 3 LeuMetTpIleThcInCys 9
 Db 6 CTAATAATGCTCTCGTCATGTC 26

RESULT 10

AZ785127

LOCUS 32 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M002811SR Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0028115 R, genomic survey sequence.

ACCESSION

AZ785127

VERSION 1
 KEYWORDS GI:12921557

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
 and Wright,D., Weils,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0028 row: 1 column: 15

Seq primer: CACACAGAAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 32.

Location/Qualifiers

1. 32

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

BASE COUNT

ORIGIN

4 a 5 c 12 g 11 t

Alignment Scores:

Pred. No.: 1.73e+04 Length: 32
 Score: 26.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 80.00% Mismatches: 0
 Query Match: 50.98% Indels: 0
 Gaps: 0

US-10-023-182-5 (1-9) x AZ785127 (1-32)

Qy 1 SerLeuMetTpIle 5

Db 18 TCATATGTTGATGTGG 32

RESULT 11

AZ478502

LOCUS 20 bp DNA linear GSS 04-OCT-2000
 DEFINITION IM0298B09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0298B09 R, genomic survey sequence.

ACCESSION

AZ478502

VERSION 1
 KEYWORDS GI:10637408

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
 and Wright,D., Weils,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0298 row: B column: 09

Seq primer: CACACAGAAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

Location/Qualifiers
1..20

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/60"
/db_xref="taxon:10090"
/clone="UUGC1M0298B09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/60 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repeated with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g[4732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

3 a 5 c 5 g 7 t

ORIGIN

Alignment Scores:

Pred. No.: 1.26e+04 Length: 20
Score: 25.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 60.00% Mismatches: 0
Query Match: 49.02% Indels: 0
DB: 28 Gaps: 0

US-10-023-182-5 (1-9) x A2478502 (1-20)

Cy 3 leuMetTpiIethr 7

Db 3 TTGCTTGGGCGACC 17

RESULT 12

BH757571

LOCUS

25 bp DNA linear GSS 01-MAR-2002
SALK_056541.20.00.x Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SALK_056541.20.00.x, genomic survey sequence.

ACCESSION

BH757571 GI:19041650

VERSION

KEYWORDS

SOURCE

ORGANISM

GSS.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; eurosid II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 25)

Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab

,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.

, Zimmerman,J., and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

unpublished

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

FEATURES

source

Email: ecker@salk.edu.
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At3g60390. Class: TDNA tagged.

Location/Qualifiers

1..25
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_056541.20.00.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT

10 a 2 c 5 g 8 t

ORIGIN

Alignment Scores:

Pred. No.: 1.77e+04 Length: 25
Score: 25.00 Matches: 3
Percent Similarity: 83.33% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 49.02% Indels: 0
DB: 28 Gaps: 0

US-10-023-182-5 (1-9) x BH757571 (1-25)

Cy 4 MetTpiIethrGlnCys 9

Db 1 ATTGGATTCCTAAGTGT 18

RESULT 13

AA466466

LOCUS

28 bp mRNA linear EST 11-JUN-1997
vg87d05.r1 Bartshead mouse pooled organs MP2RB4 Mus musculus cDNA

clone IMAGE:872937 5' similar to TR:6205858 G205858 RAT ORF.

COMPLETE CDS. //, mRNA sequence.

ACCESSION

AA466466

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 28)

Marras,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HMI Mouse EST Project

unpublished

Contact: Maria M/Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAG Consortium (info@image.jnl.gov) for further information.

MGI:512417

Trace considered overall poor quality

Possible reversed clone; similarity on wrong strand

Seq primer: -28m3 rev2 ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..28

/organism="Mus musculus"

```

/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:872937"
/sex="mixed"
/tissue_type="Pooled organs"
/dev_stage="7 day"
/lab_host="MD10B"
/clone_lib="Barstead mouse pooled organs MPRB4"
/notes="Organ: Pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site: 1: EcoRI; Site 2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACGATCTGAGTGGAGCGCGCCCTTTTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[CTTGATTCGTTACCT], digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library constructed by Bob Barstead."
BASE COUNT      2 a      8 c      8 g      9 t      1 others
ORIGIN
Alignment Scores:
Pred. No.:      2.1e+04      Length:      28
Score:          25.00      Matches:      4
Percent Similarity: 100.00%      Conservative: 1
Best Local Similarity: 80.00%      Mismatches: 0
Query Match:    49.02%      Indels:      0
DB:             9      Gaps:      0
US-10-023-182-5 (1-9) x AA46466 (1-28)
QY      1 SerLeuMetThr 5
Db      14 GCNCTTCATGCTGG 28
RESULT 14
AZ475208      28 bp      DNA      linear      GSS 04-OCT-2000
LOCUS      1M0293E18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      Clone UUGC1M0293E18 F, genomic survey sequence.
ACCESSION      AZ475208
VERSION      AZ475208.1 GI:10633333
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
JOURNAL
COMMENT      Unpublished
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0293 row: B column: 18
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
FEATURES
Source
1..28
location/Qualifiers
/mol_type="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

```

```

/clone="UUGC1M0293E18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/nares/). The DNA
was hydrodynamically sheared by repeated passages through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (GI:4732114|B|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      13 a      7 c      3 g      5 t
ORIGIN
Alignment Scores:
Pred. No.:      2.1e+04      Length:      28
Score:          25.00      Matches:      3
Percent Similarity: 83.33%      Conservative: 2
Best Local Similarity: 50.00%      Mismatches: 1
Query Match:    49.02%      Indels:      0
DB:             28      Gaps:      0
US-10-023-182-5 (1-9) x AZ475208 (1-28)
QY      2 LeuLeuMetThr 7
Db      22 CTTTTCATGCTGCA 5
RESULT 15
AZ610699      28 bp      DNA      linear      GSS 13-DEC-2000
LOCUS      1M0436L02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      Clone UUGC1M0436L02 F, genomic survey sequence.
ACCESSION      AZ610699
VERSION      AZ610699.1 GI:11732889
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
JOURNAL
COMMENT      Unpublished
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0436 row: D column: 02
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 28.

```

FEATURES

source

Location/Qualifiers

1. 28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UMC1M0436L02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10Kb plasmid UMG1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1473214|gb|AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

6 a 7 c 9 g 6 t

BASE COUNT
 ORIGIN

Alignment Scores:

Pred. No.:	2.1e+04	Length:	28
Score:	25.00	Matches:	3
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	60.00%	Mismatches:	0
Query Match:	49.02%	Indels:	0
DB:	28	Gaps:	0

US-10-023-182-5 (1-9) x AZ610699 (1-28)

QY 5 Trrplethrglncys 9
 |||:|||||
 DB 5 TGGCTTAAGGCTGC 19

Search completed: February 21, 2004, 22:51:40
 Job time : 1305.14 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2004, 17:13:46 ; Search time 2035.24 Seconds
(without alignments)
180.906 Million cell updates/sec

Title: US-10-023-182-6
Perfect score: 46
Sequence: 1 QLSLMMIT 9

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481336 residues
Total number of hits satisfying chosen parameters: 1074678

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=x1h
-Q=cm2.1/USPRO.spool/US10023182/runat.20022004.11043.21319/app.query.fasta.1.597
-DB=GenBdb1 -QPM=fastap -SUFFIX=5ge -MITMATCH=0.1 -LOOFCU=0 -LOOEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPM=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=33
-USR=US10023182 @CGN 1.1 3707 @runat.20022004.11043.21319 -NCPU=6 -ICPU=3
-NO_MMAP -IARGOUTERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmb1.*
1: gb_ba:*
2: gb_hhg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_ov:*
23: em_ph:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	69.6	19	AR042534	AR042534 Sequence
2	32	69.6	30	E09921	E09921 PCR Primer
3	31	67.4	27	AR082630	AR082630 Sequence
4	31	67.4	30	AB1186	AB1186 Sequence 10
5	31	67.4	33	AR040591	AR040591 Sequence
6	31	67.4	33	AR055615	AR055615 Sequence
7	30	65.2	22	AB1187	AB1187 Sequence 11
8	30	65.2	28	AR161714	AR161714 Sequence
9	30	65.2	28	AR205630	AR205630 Sequence
10	29	63.0	20	AR271895	AR271895 Sequence
11	29	63.0	21	AX024699	AX024699 Sequence
12	29	63.0	30	BD014427	BD014427 Method fo
13	29	63.0	31	I45554	I45554 Sequence 3
14	29	63.0	31	I45555	I45555 Sequence 4
15	28	60.9	17	AX127827	AX127827 Sequence
16	28	60.9	17	AX733091	AX733091 Sequence
17	28	60.9	17	AX733203	AX733203 Sequence
18	28	60.9	18	BD000827	BD000827 Method of
19	28	60.9	18	I50911	I50911 Sequence 5
20	28	60.9	18	I83439	I83439 Sequence 3
21	28	60.9	20	AR295082	AR295082 Sequence
22	28	60.9	26	AX465553	AX465553 Sequence
23	28	60.9	26	AX642859	AX642859 Sequence
24	28	60.9	26	AX703159	AX703159 Sequence
25	28	60.9	29	AX163906	AX163906 Sequence
26	28	60.9	29	AX163914	AX163914 Sequence
27	28	60.9	29	AX163928	AX163928 Sequence
28	28	60.9	29	AX195469	AX195469 Sequence
29	28	60.9	29	BD107031	BD107031 Process f
30	28	60.9	29	E59689	E59689 Ribosome re
31	27	58.7	20	AR114241	AR114241 Sequence
32	27	58.7	21	AR141564	AR141564 Sequence
33	27	58.7	21	AX018516	AX018516 Sequence
34	27	58.7	21	AX018592	AX018592 Sequence
35	27	58.7	21	BD136254	BD136254 Enhance
36	27	58.7	23	AR091414	AR091414 Sequence
37	27	58.7	23	AR125619	AR125619 Sequence
38	27	58.7	23	AR308289	AR308289 Sequence
39	27	58.7	23	AX029046	AX029046 Sequence
40	27	58.7	23	AX286791	AX286791 Sequence
41	27	58.7	23	BD009331	BD009331 Viral Var
42	27	58.7	24	AR088606	AR088606 Sequence
43	27	58.7	24	AR088607	AR088607 Sequence
44	27	58.7	24	AR183396	AR183396 Sequence
45	27	58.7	24	AR183397	AR183397 Sequence

RESULT 1

ALIGNMENTS

```

AR042534/c
LOCUS AR042534 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 581519.
ACCESSION AR042534
VERSION AR042534.1 GI:5963030
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 19)
  Leche,B., Lucas,S., De Smet,C., Godelaine,D. and Boon-Falleur,T.
  IL-1 tumor specific genes
  JOURNAL Patent: US 581519-A 3 22-SEP-1998;
  TITLE Location/Qualifiers
  FEATURES
    source 1..19
    /organism="unknown"
BASE COUNT 8 a 5 c 4 g 2 t
ORIGIN
Alignment Scores:
Pred. No.: 111 Length: 19
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.57% Indels: 0
Gaps: 0
DB: 6
US-10-023-182-6 (1-9) x AR042534 (1-19)

Qy 3 SerLeuLeuMetTyrPle 8
Db 18 TCCTGTGATGTGATC 1

RESULT 2
LOCUS E09921 30 bp DNA linear PAT 29-SEP-1997
DEFINITION PCR primer for gaining human albumin.
ACCESSION E09921
VERSION E09921.1 GI:22026549
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 30)
  Beppu,T., Horinouchi,S. and Nomura,N.
  FUSION GENE HAVING ALBUMIN GENE AND HUMAN APOLIPOPROTEIN GENE,
  PLASMID INCLUDING THE GENE AND ITS USE
  JOURNAL Patent: JP 1995241196-A 1 19-SEP-1995;
  TITLE BEPPU TERUHIKO
  FEATURES
    OS None
    OC Artificial sequences.
    PD JP 1995241196-A/1
    PN 19-SEP-1995
    PF 04-MAR-1994 JP 1994058270
    PI BEPPU TERUHIKO, HORINOUCHI SUEI, NOMURA NOBUHIKO PC
    CI1N15/09 CI2N1/19, CI2P21/02//A6IK36/00, (CI2N15/09, CI2R1:645), PC
    (CI2N1/19)
    PC CI2R1:645), (CI2P21/02, CI2R1:645);
    CC strandedness: single;
    CC topology: linear;
    FH Key Location/Qualifiers
    FT source 1..30
    misc_feature 3..8 /note='HindIII digestion site'.
  FT
  Location/Qualifiers
  1..30
  /organism="unidentified"
  /mol_type="genomic DNA"
  /db_xref="taxon:32644"
BASE COUNT 9 a 4 c 6 g 11 t
ORIGIN

```

```

Alignment Scores:
Pred. No.: 167 Length: 30
Score: 32.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 69.57% Indels: 0
Gaps: 6
US-10-023-182-6 (1-9) x E09921 (1-30)

Qy 2 LeuSerLeuLeuMetTyrPleThr 9
Db 1 CTAAAGCTTAATGAAGTGGGTAAACC 24

RESULT 3
LOCUS AR082630 27 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 13 from patent US 5973228.
ACCESSION AR082630
VERSION AR082630.1 GI:10009350
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 27)
  Carlson,J.E., Dharmawardhana,D.Palitha., Douglas,C.J. and
  Ellis,B.E.
  Conferrin beta-glucosidase cDNA for modifying lignin content in
  JOURNAL Patent: US 5973228-A 13 26-OCT-1999;
  TITLE Location/Qualifiers
  FEATURES
    source 1..27
    /organism="unknown"
BASE COUNT 4 a 1 c 12 g 10 t
ORIGIN
Alignment Scores:
Pred. No.: 248 Length: 27
Score: 31.00 Matches: 4
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 0
Query Match: 67.39% Indels: 0
Gaps: 0
DB: 6
US-10-023-182-6 (1-9) x AR082630 (1-27)

Qy 1 GinLeuSerLeuLeuMetTyrPle 8
Db 4 GAGGTCTCTGTGTGATGTGGGTA 27

RESULT 4
LOCUS A81186/c 30 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 10 from Patent WO9914323.
ACCESSION A81186
VERSION A81186.1 GI:6731645
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 30)
  Mueller,H. and Eppenberger,U.
  HERRGULIN-GAMMA
  JOURNAL Patent: WO 9914323-A 10 25-MAR-1999;
  TITLE MUELLER HEINZ (CH); EPPENBERGER URS (CH)
  JOURNAL
  FEATURES
    source 1..30
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
BASE COUNT 12 a 6 c 8 g 4 t
ORIGIN

```


Alignment Scores:
 Pred. No.: 272 Length: 30
 Score: 31.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 3
 Best Local Similarity: 62.50% Mismatches: 0
 Query Match: 67.39% Indels: 0
 DB: 6 Gaps: 0

US-10-023-182-6 (1-9) x AB1186 (1-30)

QY 2 LeuSerLeuMetTyrPile 9
 Db 25 TTGAGCCTTCTTGTGATATCG 2

RESULT 5 AR040591/c AR040591 33 bp DNA 1 linear PAT 29-SEP-1999
 LOCUS Sequence 61 from patent US 5807824.
 DEFINITION AR040591
 ACCESSION AR040591
 VERSION AR040591.1 GI:5959954
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
 AUTHORS van Oostrum,J., Boyar,W.C., Galakatos,N.G., Schmitz,A. and Van Heeke,G.
 TITLE CSA receptor antagonists having substantially no agonist activity
 JOURNAL Patent: US 5807824-A 61.15-SEP-1999;
 FEATURES Location/Qualifiers

source 1..33
 /organism="unknown"

BASE COUNT 11 a 6 c 9 g 7 t
 ORIGIN

Alignment Scores:
 Pred. No.: 297 Length: 33
 Score: 31.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 71.43% Mismatches: 0
 Query Match: 67.39% Indels: 0
 DB: 6 Gaps: 0

US-10-023-182-6 (1-9) x AR040591 (1-33)

QY 2 LeuSerLeuMetTyrPile 8
 Db 28 TTGAGCCTCATGCTGTGATC 8

RESULT 6 AR055615/c AR055615 33 bp DNA 1 linear PAT 29-SEP-1999
 LOCUS Sequence 61 from patent US 5837499.
 DEFINITION AR055615
 ACCESSION AR055615
 VERSION AR055615.1 GI:5981192
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
 AUTHORS van Oostrum,J., Boyar,W.C., Galakatos,N.G., Schmitz,A. and Van Heeke,G.
 TITLE DNA encoding CSA receptor antagonists having substantially no agonist activity and methods of expressing same
 JOURNAL Patent: US 5837499-A 61.17-NOV-1998;
 FEATURES Location/Qualifiers

source 1..33
 /organism="unknown"

BASE COUNT 11 a 6 c 9 g 7 t
 ORIGIN

Alignment Scores:

Pred. No.: 297 Length: 33
 Score: 31.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 71.43% Mismatches: 0
 Query Match: 67.39% Indels: 0
 DB: 6 Gaps: 0

US-10-023-182-6 (1-9) x AR055615 (1-33)

QY 2 LeuSerLeuMetTyrPile 8
 Db 28 TTGAGCCTCATGCTGTGATC 8

RESULT 7 AB1187 AB1187 22 bp DNA 1 linear PAT 21-JAN-2000
 LOCUS Sequence 11 from Patent WO9914323.
 DEFINITION AB1187
 ACCESSION AB1187
 VERSION AB1187.1 GI:6731646
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Mueller,H. and Eppenberger,U.
 TITLE HERGULIN-GAMMA
 JOURNAL Patent: WO 9914323-A 11.25-MAR-1999;
 FEATURES Location/Qualifiers

source 1..22
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

BASE COUNT 2 a 6 c 4 g 10 t
 ORIGIN

Alignment Scores:
 Pred. No.: 334 Length: 22
 Score: 30.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 71.43% Mismatches: 0
 Query Match: 65.22% Indels: 0
 DB: 6 Gaps: 0

US-10-023-182-6 (1-9) x AB1187 (1-22)

QY 2 LeuSerLeuMetTyrPile 8
 Db 2 CTGGCCTTCTTGTGATC 22

RESULT 8 AR161714/c AR161714 28 bp DNA 1 linear PAT 17-OCT-2001
 LOCUS Sequence 24 from patent US 6258529.
 DEFINITION AR161714
 ACCESSION AR161714
 VERSION AR161714.1 GI:16228605
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 28)
 AUTHORS Berdoz,J. and Kraehenbuhl,J.-P.
 TITLE PCR amplification of rearranged genomic variable regions of immunoglobulin genes

JOURNAL Patent: US 6258529-A 24.10-JUL-2001;
 FEATURES Location/Qualifiers

source 1..28
 /organism="unknown"

BASE COUNT 8 a 7 c 10 g 3 t
 ORIGIN

Alignment Scores: 416 Length: 28

Score: 30.00 Matches: 5
 Percent Similarity: 87.50% Conservative: 2
 Best Local Similarity: 62.50% Mismatches: 1
 Query Match: 65.22% Indels: 0
 DB: 6 Gaps: 0

US-10-023-182-6 (1-9) x AR161714 (1-28)

Qy 2 LeuSerLeuMetTrpIleThr 9
 Db 27 ATGTCCCTCTGCTGCTGCTGACG 4

RESULT 9
 LOCUS AR205630/c 28 bp DNA linear PAT 20-JUN-2002
 DEFINITION Sequence 12 from patent US 6365195.
 ACCESSION AR205630
 VERSION AR205630.1 GI:21503262
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Au, G. and Veltri, R.
 TITLE Prostate-specific gene for diagnosis, prognosis and management of prostate cancer
 JOURNAL Patent: US 6369195-A 12 09-APR-2002;
 FEATURES Location/Qualifiers
 source 1..28
 /organism="unknown"

BASE COUNT 10 a 7 c 7 g 4 t
 ORIGIN

Alignment Scores:
 Pred. No.: 416 Length: 28
 Score: 30.00 Matches: 5
 Percent Similarity: 87.50% Conservative: 2
 Best Local Similarity: 62.50% Mismatches: 1
 Query Match: 65.22% Indels: 0
 DB: 6 Gaps: 0

US-10-023-182-6 (1-9) x AR205630 (1-28)

Qy 2 LeuSerLeuMetTrpIleThr 9
 Db 26 CTTTCATCTCTGCTGATGACG 3

RESULT 10
 LOCUS AR271895/c 20 bp DNA linear PAT 10-APR-2003
 DEFINITION Sequence 139 from patent US 6503754.
 ACCESSION AR271895
 VERSION AR271895.1 GI:29703463
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Zhang, H. and Wyatt, J.
 TITLE Antisense modulation of B33 interacting domain death agonist
 JOURNAL Expression Patent: US 6503754-A 139 07-JAN-2003;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"

BASE COUNT 8 a 5 c 6 g 1 t
 ORIGIN

Alignment Scores:
 Pred. No.: 499 Length: 20
 Score: 29.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 83.33% Mismatches: 0

Query Match: 63.04% Indels: 0
 DB: 6 Gaps: 0

US-10-023-182-6 (1-9) x AR271895 (1-20)

Qy 2 LeuSerLeuMetTrp 7
 Db 20 CTCAGTCTCTCTGTGG 3

RESULT 11
 LOCUS AX024699/c 21 bp DNA linear PAT 15-SEP-2000
 DEFINITION Sequence 15 from Patent EP1001022.
 ACCESSION AX024699
 VERSION AX024699.1 GI:10184783
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Aarnoudse, C.A. and Schrier, P.
 TITLE Camel, an alternative translation product of the tumour antigen
 JOURNAL Patent: EP 1001022-A 15 17-MAY-2000;
 FEATURES Location/Qualifiers
 source 1..21
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Primer"

BASE COUNT 6 a 7 c 4 g 4 t
 ORIGIN

Alignment Scores:
 Pred. No.: 521 Length: 21
 Score: 29.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 63.04% Indels: 0
 DB: 6 Gaps: 0

US-10-023-182-6 (1-9) x AX024699 (1-21)

Qy 5 LeuMetTrpIleThr 9
 Db 21 TTGATGATGATCAAG 7

RESULT 12
 LOCUS BD014427/c 30 bp DNA linear PAT 27-AUG-2002
 DEFINITION Method for formation of virus-like particles from VP3 capsid
 ACCESSION BD014427
 VERSION BD014427.1 GI:22555210
 KEYWORDS
 SOURCE Simian virus 40
 ORGANISM Simian virus 40
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Henda, H., Hock, M., Ishizu, K. and Watanabe, H.
 TITLE Method for formation of virus-like particles from VP3 capsid
 JOURNAL Protein of adeno-associated virus
 Patent: JP 2001169777-A 7 26-JUN-2001;
 COMMENT HIROSHI HANDA
 OS SV40
 PN JP 2001169777-A/7
 PD 26-JUN-2001
 PF 30-JUL-1999 JP 1999249140
 PI HIROSHI HANDA, MYNOBU HOCK, KENICHIRO ISHIZU, HAJIME WATANABE
 C12N15/00, C07K14/075, C12N5/10, C12N7/00, C12N1/00, C12R1/92, PC
 C12N15/00, PC
 C12N5/00

CC Nucleotide sequence coding for nuclear location signal- CC
 CC of SV40 large T antigen
 FH Key Location/Qualifiers
 FEATURES
 source 1..30
 /organism="Simian virus 40"
 /mol_type="genomic DNA"
 /db_xref="taxon:10633"
 BASE COUNT 13 a 6 c 8 g 3 t
 ORIGIN

Alignment Scores:
 Pred. No.: 720 Length: 30
 Score: 29.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 83.33% Mismatches: 0
 Query Match: 63.04% Indels: 0
 DB: 6 Gaps: 0

US-10-023-182-6 (1-9) x BD014427 (1-30)

QY 2 LeuSerLeuMetTrp 7
 DB 27 CTTTCCTCTCTCTTGG 10

RESULT 13
 LOCUS 145554 31 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 3 from patent US 5637463.
 ACCESSION 145554
 VERSION 145554.1 GI:2469656
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 31)
 AUTHORS Dalton,S., Kochan,J.P. and Osborne,M.A.
 TITLE Method to detect protein-protein interactions
 JOURNAL Patent: US 5637463-A 3 10-JUN-1997;
 FEATURES
 source 1..31
 /organism="unknown"
 BASE COUNT 12 a 6 c 12 g 1 t
 ORIGIN

Alignment Scores:
 Pred. No.: 742 Length: 31
 Score: 29.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 83.33% Mismatches: 0
 Query Match: 63.04% Indels: 0
 DB: 6 Gaps: 0

US-10-023-182-6 (1-9) x 145554 (1-31)

QY 2 LeuSerLeuMetTrp 7
 DB 25 CTTTCCTCTCTTGG 8

RESULT 14
 LOCUS 145555 31 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 4 from patent US 5637463.
 ACCESSION 145555
 VERSION 145555.1 GI:2469657
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 31)
 AUTHORS Dalton,S., Kochan,J.P. and Osborne,M.A.
 TITLE Method to detect protein-protein interactions

JOURNAL Patent: US 5637463-A 4 10-JUN-1997;
 FEATURES
 source 1..31
 /organism="unknown"
 BASE COUNT 3 a 10 c 4 g 14 t
 ORIGIN

Alignment Scores:
 Pred. No.: 742 Length: 31
 Score: 29.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 83.33% Mismatches: 0
 Query Match: 63.04% Indels: 0
 DB: 6 Gaps: 0

US-10-023-182-6 (1-9) x 145555 (1-31)

QY 2 LeuSerLeuMetTrp 7
 DB 11 CTTTCCTCTCTTGG 28

RESULT 15
 LOCUS AX727827 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 5514 from Patent WO03025176.
 ACCESSION AX727827
 VERSION AX727827.1 GI:30507170
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Tejeraman,A., Amson,R. and Tuijinder,M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour
 reversion, apoptosis and/or virus resistance and their use as
 medicines
 JOURNAL Patent: WO 03025176-A 5514 27-MAR-2003;
 FEATURES
 source 1..17
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 BASE COUNT 6 a 3 c 5 g 3 t
 ORIGIN

Alignment Scores:
 Pred. No.: 700 Length: 17
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 60.87% Indels: 0
 DB: 6 Gaps: 0

US-10-023-182-6 (1-9) x AX727827 (1-17)

QY 4 LeuLeuMetTrpIle 8
 DB 15 CTCCTCATGTGATC 1

Search completed: February 21, 2004, 21:41:31
 Job time : 2037.24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: February 21, 2004, 13:32:10 (Search time 171 Seconds)

(without alignments)
142.076 Million cell updates/sec

Title: US-10-023-182-6

Perfect score: 46
Sequence: 1 QSLMMIT 9

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2197996

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=X1h
-Q=/cgn2.1/USPTO.spool/US10023182/runatc_20022004.111042.21309/app.query.fasta_1.597
-DB=N Geneseq 19Jun03 -OPMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=p2n -NOEM=ext -HEAPSIZE=500 -MNTLEN=0 -MAXLEN=33
-USPR=US10023182 @CEN 1.1.0 @runatc_20022004.111042.21309 -NCPU=6 -ICPU=3
-NO MMAP -LARGESUBSTRY -NEG_SCORES=0 -WAIT -DEPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WASN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 19Jun03:

1: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1980.DAT:*
2: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1981.DAT:*
3: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1982.DAT:*
4: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1983.DAT:*
5: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1984.DAT:*
6: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1985.DAT:*
7: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1986.DAT:*
8: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1987.DAT:*
9: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1988.DAT:*
10: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1989.DAT:*
11: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1990.DAT:*
12: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1991.DAT:*
13: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1992.DAT:*
14: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1993.DAT:*
15: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1994.DAT:*
16: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1995.DAT:*
17: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1996.DAT:*
18: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1997.DAT:*
19: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1998.DAT:*
20: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA1999.DAT:*
21: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA2000.DAT:*
22: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA2001.DAT:*
23: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA2002.DAT:*
24: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA2003.DAT:*
25: /SIDSI/gcgdata/geneseg/geneseg-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	32	69.6	19	AAV50351	Human LAGE-1 PCR p
C 2	32	69.6	30	AAV50351	Human albumin/apol
C 3	31	67.4	24	AAV50351	Large T antigen nu
C 4	31	67.4	27	AAV50351	Conferrin beta glu
C 5	31	67.4	33	AAV50351	PCR primer for pla
C 6	30	65.2	28	AAV50351	Primer 5'kappall f
C 7	30	65.2	28	AAV50351	PCR primer used to
C 8	30	65.2	33	AAV50351	Probe for human SH
C 9	30	65.2	33	AAV50351	Human acyl CoA syn
C 10	29	63.0	20	AAV50351	Mouse BH3 interact
C 11	29	63.0	21	AAV50351	Reverse PCR primer
C 12	29	63.0	30	AAV50351	SV40 large T antig
C 13	29	63.0	30	AAV50351	Novel Helicobacter
C 14	29	63.0	31	AAV50351	SV40 T antigen nuc
C 15	29	63.0	31	AAV50351	Human genomic DNA
C 16	29	63.0	31	AAV50351	Human lipase 37 PC
C 17	29	63.0	33	AAV50351	Tumour suppression
C 18	28	60.9	17	AAV50351	Tumour suppression
C 19	28	60.9	17	AAV50351	Primer 22-CST3 fo
C 20	28	60.9	20	AAV50351	Human biallelic ma
C 21	28	60.9	20	AAV50351	Human SHP-2 antise
C 22	28	60.9	20	AAV50351	Human hpa cDNA fra
C 23	28	60.9	22	AAV50351	PCR primer used to
C 24	28	60.9	22	AAV50351	PCR primer used to
C 25	28	60.9	23	AAV50351	Chitinase specific
C 26	28	60.9	24	AAV50351	Human G-protein co
C 27	28	60.9	26	AAV50351	Novel G-protein co
C 28	28	60.9	26	AAV50351	Cytochrome p450 no
C 29	28	60.9	26	AAV50351	Halobacterium sal
C 30	28	60.9	29	AAV50351	human-Hs EcOR1/nde
C 31	28	60.9	29	AAV50351	Primer #1, co crea
C 32	28	60.9	29	AAV50351	T. thermophilus xi
C 33	28	60.9	29	AAV50351	Novel Helicobacter
C 34	28	60.9	29	AAV50351	PCR primer used to
C 35	28	60.9	30	AAV50351	Cryptosporidium pa
C 36	27	58.7	21	AAV50351	Simian virus 40 (S
C 37	27	58.7	21	AAV50351	SV40 nuclear local
C 38	27	58.7	21	AAV50351	Human DSPR PCR pri
C 39	27	58.7	21	AAV50351	Mason-Pfizer monke
C 40	27	58.7	21	AAV50351	DNA polymerase var
C 41	27	58.7	23	AAV50351	Nucleic acid trans
C 42	27	58.7	23	AAV50351	Target sequence in
C 43	27	58.7	23	AAV50351	HBV DNA polymerase
C 44	27	58.7	23	AAV50351	
C 45	27	58.7	23	AAV50351	

ALIGNMENTS

RESULT 1
AAV50351/c
ID AAV50351 standard; cDNA; 19 BP.
AC AAV50351;
XX 27-OCT-1998 (first entry)
XX Human LAGE-1 PCR primer B1556.
XX Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour;
XX PCR primer; ss.
XX Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour;
XX Synthetic.
XX Homo sapiens.
XX WO9832855-A1.
FN

XX 30-JUL-1998.
 PD 27-JUN-1998; 98WO-US01445.
 XX 27-JUN-1997; 97US-0791495.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA Boon-Fallieur T, De Smet C, Godelaine D, Iethe B;
 PI Lucas S;
 XX WPI; 1998-427951/36.
 DR
 PT New isolated LAGE-1 tumour associated nucleic acids - used to
 PT develop products for the diagnosis and treatment of LAGE-1
 PT associated disorders, particularly tumours
 XX Example 1; Page 50; 73pp; English.
 PS
 CC The present sequence represents a PCR primer for LAGE-1 tumour
 CC associated protein (TAP). The present invention also describes: (1) a
 CC method for treating a subject with a disorder characterized by
 CC expression of a LAGE-1 nucleic acid molecule or an expression product,
 CC comprising administering to the subject autologous cytolytic T cells to
 CC ameliorate the disorder, where the cytolytic T cells are specific for
 CC complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic
 CC fragment; (2) a method for treating a subject with a disorder
 CC characterized by expression of a LAGE-1 nucleic acid molecule or an
 CC expression product, comprising administering a LAGE-1 TAP or an
 CC immunogenic fragment to ameliorate the disorder; and (3) a method for
 CC selectively enriching a population of T cells with cytolytic T cells
 CC specific for a LAGE-1 TAP comprising contacting an isolated population
 CC of T cells with an agent presenting a complex of a LAGE TAP or an
 CC immunogenic fragment and a HLA presenting molecule to selectively
 CC enrich the isolated population of T cells with the cytolytic T cells.
 CC The methods and products from the present invention can be used for the
 CC diagnosis and treatment of LAGE-1 associated disorders, particularly
 CC tumours.
 CC
 SQ Sequence 19 BP; 8 A; 5 C; 4 G; 2 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 135 Length: 19
 Score: 32.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 69.57% Indels: 0
 DB: 19 Gaps: 0
 US-10-023-182-6 (1-9) x AAV50351 (1-19)
 QY 3 SerLeuLeuMeTrrIle 8
 DB 18 TCCCTGTGATGCGATC 1
 RESULT 2
 AAT09051
 ID AAT09051 standard; DNA; 30 BP.
 XX AAT09051;
 AC
 XX 14-MAY-1996 (first entry)
 DT
 XX Human albumin/apolipoprotein fusion protein primer #1.
 DE
 XX Primer; PCR, amplification; fusion protein; human; albumin; reagent;
 KM apolipoprotein E; yeast; S.cerevisiae; intermediate; drug; ss.
 XX Synthetic.
 OS
 XX JP07241196-A.
 XX PN
 XX

PD 19-SEP-1995.
 XX 04-MAR-1994; 94JP-0058270.
 XX 04-MAR-1994; 94JP-0058270.
 XX (BEPP/) BEPPU T.
 PA WPI; 1995-354277/46.
 DR
 XX Fusion gene coding for albumin fused to human apolipoprotein E -
 PT also vectors and transformed yeast for prep. of fusion protein as
 PT intermediate for drugs, reagents and apolipoprotein B
 XX Example 1; Page 9; 12pp; Japanese.
 PS
 CC Primers AAT09051-63 are used to produce a novel fusion protein
 CC consisting of the human albumin linked N-terminally to the human
 CC apolipoprotein E. The primers AAT09051-2 were used to amplify the
 CC complete human albumin gene and corresp. to sequences in the N-terminus
 CC and C-terminus resp. The resultant fragment was cloned into the plasmid
 CC pUC19 to produce plasmid pABE1. The fusion gene is cloned into a yeast
 CC plasmid and expressed in S.cerevisiae. The fusion protein is useful as
 CC an intermediate for the synthesis of reagents, drugs and apolipoprotein
 CC E-like proteins.
 CC
 SQ Sequence 30 BP; 9 A; 4 C; 6 G; 11 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 225 Length: 30
 Score: 32.00 Matches: 5
 Percent Similarity: 87.50% Conservative: 2
 Best Local Similarity: 62.50% Mismatches: 1
 Query Match: 69.57% Indels: 0
 DB: 16 Gaps: 0
 US-10-023-182-6 (1-9) x AAT09051 (1-30)
 QY 2 LeuSerLeuLeuMeTrrIleThr 9
 DB 1 CTAAGCTTAATGAAGTGGGTAAAC 24
 RESULT 3
 AAA93915/C
 ID AAA93915 standard; DNA; 24 BP.
 XX AAA93915;
 AC
 XX 15-JAN-2001 (first entry)
 DT
 XX Large T antigen nuclear localisation signal 3 tandem repeat sequence.
 DE
 XX Nuclear localisation signal; large T-antigen; target molecule screening;
 KM tetracycline-inducible system; antisense molecule; ribosome; antibody;
 KM receptor; cytokine; angiogenesis modulator; growth hormone; ds.
 XX Simian virus.
 OS
 XX WO20005378-A1.
 XX 21-SEP-2000.
 PD
 XX 16-MAR-2000; 2000MO-US07064.
 PF
 XX 16-MAR-1999; 99US-0124641.
 PR
 XX (DAND) DANA FARBER CANCER INST INC.
 PA Marasco WA, Ogata S;
 PI WPI; 2000-602130/57.
 DR
 XX Screening a target molecule such as an antibody, receptor, or hormone
 PT

PT from a group of target molecules, by transducing cells with a library
 of lentiviral vectors and screening the transduced cell for desired the
 phenotype

PS Example 5; Page 31, 70pp; English.

CC This sequence represents a three tandem repeat sequence of the nuclear
 CC localisation signal from simian virus large T-antigen. The sequence is
 CC used in the construction of a single-plasmid tetracycline-inducible
 CC system. The single plasmid system is used in an example of a method for
 CC screening for a target molecule from a group of target molecules. The
 CC method comprises transducing a group of cells with a library of
 CC lentiviral vectors, where the members encode the group of target
 CC molecules, and screening the transduced cells for a desired phenotype.
 CC The method is useful for screening target molecules such as an antisense
 CC molecule, a ribozyme, an antibody, a receptor, a cytokine, an
 CC angiogenesis modulator or a growth hormone, from a group of target
 CC molecules. The target molecule is preferably an antibody adapted for
 CC expression and binding within a cell or a ribozyme or antisense molecule
 CC capable of transplanning.

CC Sequence 24 BP, 14 A, 2 C, 6 G, 2 T, 0 other;

SO

Alignment Scores:

Pred. No.:	269	Length:	24
Score:	31.00	Matches:	6
Percent Similarity:	85.71%	Conservative:	0
Best Local Similarity:	85.71%	Mismatches:	1
Query Match:	67.39%	Indels:	0
DB:	21	Gaps:	0

US-10-023-182-6 (1-9) x AAV36589 (1-24)

OY 2 LeuserleuMectrpile 8

DB 21 CTTCTCTCTCTTTTGATC 1

RESULT 4

AAV36589 standard; DNA; 27 BP.

AC AAV36589;

XX 02-OCT-1998 (first entry)

DE Coniferin beta-glucosidase (CBG) cDNA amplifying primer 3.

XX Coniferin beta-glucosidase; Pinus contorta; transgenic plant;

KW conifer; pine; lignin; papermaking; CBG; PCR primer; ss.

OS Synthetic.

OS Pinus contorta.

XX NZ28434-A.

XX 27-MAY-1998.

XX 25-JUL-1997; 97NZ-0328434.

XX 25-JUL-1997; 97NZ-0328434.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Carlson JE, Dharmawardhana DP, Douglas CJ, Ellis BE;

XX WPI; 1998-360312/31.

PT DNA encoding coniferin beta-glucosidase enzyme - for producing

XX transgenic plants with altered lignin content

XX Example 4; Page 26; 77pp; English.

CC This primer is used for the PCR amplification of the cDNA encoding a

CC coniferin beta-glucosidase (CBG) enzyme. The CBG gene is used in the
 CC method of inventing of producing a transgenic plant with altered lignin
 CC content. The method comprises introducing into the plant a recombinant
 CC vector containing a promoter operably linked to a coding sequence which
 CC encodes an untranslatable plus-sense transcript that shares at least 80
 CC percent sequence similarity with a transcript of a native CBG gene.
 CC Antisense coniferin beta-glucosidase nucleic acid sequence can also be
 CC used to produce a transgenic plant with altered lignin content, which
 CC when expressed in cells of the plant, inhibits expression of a native
 CC CBG gene. The products and methods can be used to produce plants with a
 CC reduced lignin content, preferably conifers, especially pines. Wood from
 CC trees with a reduced lignin content would facilitate paper making.

SO Sequence 27 BP, 4 A, 1 C, 12 G, 10 T, 0 other;

Alignment Scores:

Pred. No.:	307	Length:	27
Score:	31.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	50.00%	Mismatches:	0
Query Match:	67.39%	Indels:	0
DB:	19	Gaps:	0

US-10-023-182-6 (1-9) x AAV36589 (1-27)

OY 1 GluserleuMectrpile 8

DB 4 GAGGTCTCTCTTTGATGCGTA 27

RESULT 5

AAAT47213/c

ID AAAT47213 standard; DNA; 33 BP.

AC AAAT47213;

XX 01-SEP-1997 (first entry)

DE PCR primer for plasmid pPMLuIL72.

XX Human; interleukin 1; beta; receptor; IL72; antagonist; hybrid;

KW fusion; polymerase chain reaction; PCR; amplification; plasmid;

XX pPMLuIL72; ss.

OS Synthetic.

XX WO9639503-A1.

XX 12-DEC-1996.

XX 04-JUN-1996; 96WO-EP02422.

XX 05-JUN-1995; 95US-0463377.

XX 05-JUN-1995; 95US-0462548.

XX 05-JUN-1995; 95US-0463224.

XX (CIBA) CIBA GEIGY AG.

XX Schmitz A, Van Heeke G, Van Oostrum J;

XX WPI; 1997-043125/04.

PT New human complement C5a poly-peptide derivs. - used as C5a receptor

XX antagonists, partic. for treating C5a-mediated diseases and

XX inflammatory conditions

XX Example 17; Page 46; 93pp; English.

CC The present sequence is a primer for the PCR amplification of the

CC plasmid pPMLuIL72, which contains the DNA sequence of IL72 flanked

CC by NcoI and GamHI restriction sites. IL72 is a hybrid protein

CC composed of human interleukin 1 beta and human interleukin 1

CC receptor antagonist.

SQ Sequence 33 BP; 11 A; 6 C; 9 G; 7 T; 0 other;

Alignment Scores:

Pred. No.:	Length:
Score: 31.00	Matches: 33
Percent Similarity: 100.00%	Conservative: 5
Best Local Similarity: 71.43%	Mismatches: 0
Query Match: 67.39%	Indels: 0
DB: 18	Gaps: 0

US-10-023-182-6 (1-9) x AAT47213 (1-33)

QY 2 LeuSerLeuMetTyrPhe 8

DB 28 TTGAGCCTCATGCTGTGATC 8

RESULT 6

AT30474/c

AT30474 standard; DNA; 28 BP.

AC AAT30474;
AT 11-FEB-1997 (first entry)
DE Primer 5'kappal1 for HNK-20 V kappa chain coding sequence.

XX Antibody; HNK-20, variable kappa chain, hybridoma; murine; IgA; mouse;
XX F glycoprotein; respiratory syncytial virus; RSV; constant region gene;
XX chimeric antibody; isotype-switched antibody; therapy; infection; human;
XX pneumonia; bronchiolitis; animal; polymerase chain reaction; primer; PCR;
XX amplify; ss.

OS Synthetic.

PN WO9616974-A1.

PD 06-JUN-1996.

PF 01-DEC-1995; 95WO-US15716.

PR 01-DEC-1994; 94US-0346548.

PA (ORAV-) ORAVAX INC.

PI Berdoz J, Kraehenbuhl J;

DR WPI; 1996-286826/29.

PT DNA encoding variable region of antibody HNK-20 - for treating
PT respiratory syncytial virus infection

PS Example; Page 36; 75pp; English.

XX AAT30459-730545 represent amplification primers for the coding sequences
XX for the variable chains of an antibody produced by the hybridoma cell
XX line HNK-20. AAT30464-730498 represent amplification primers for the
XX coding sequence for the variable kappa chain of the HNK-20 antibody.
XX HNK-20 is a murine hybridoma cell line, that produces IgA specific for
XX the F glycoprotein of respiratory syncytial virus (RSV). The variable
XX chain coding sequences (see AAT30456-730456) were isolated using primers
XX specific for the 5' untranslated region of the variable region, and for
XX the intron downstream of the rearranged J region. The amplified
XX sequences can be inserted into vectors containing heterologous (such as
XX human) constant region genes, for the production of chimeric and
XX isotype-switched antibodies. The antibodies are useful in the treatment
XX and diagnosis of infection by RSV, such as pneumonia and bronchiolitis,
XX in humans and animals. By using genomic DNA as a template, variable
XX region genes can be isolated without producing fragments that have to be
XX adapted for recombinant antibody expression. Also, by using the genomic
XX DNA, no knowledge of the DNA sequence encoding the target variable
XX region is required. Chimeric antibodies produced from the encoded
XX proteins, that contain the constant region of the host being treated, are
XX less likely to cause adverse immune reactions.

XX SQ Sequence 28 BP; 8 A; 7 C; 10 G; 3 T; 0 other;

Alignment Scores:

Pred. No.:	Length:
Score: 489	Matches: 28
Percent Similarity: 30.00	Conservative: 5
Best Local Similarity: 87.50%	Mismatches: 2
Query Match: 62.50%	Indels: 1
DB: 17	Gaps: 0

US-10-023-182-6 (1-9) x AAT30474 (1-28)

QY 2 LeuSerLeuMetTyrPheThr 9

DB 27 ATGTCCTGCTGCTGTGTCGACG 4

RESULT 7

AA63808/c

AA63808 standard; cDNA; 28 BP.

AC AA63808;
AT 04-DEC-2000 (first entry)
DE PCR primer used to amplify human beta2-microglobulin cDNA sequences.

XX Prostate specific protein; UC41; prostate cancer; prostate cancer marker;
XX PCR primer; ss.
XX Homo sapiens.

OS Homo sapiens.

PN WO20004773-A1.

PD 17-AUG-2000.

PF 24-JAN-2000; 2000WO-US02052.

PR 09-FEB-1999; 99US-0247188.

PA (UROC-) UROCOR INC.

PI An G, Veltri R;

DR WPI; 2000-515061/46.

PT New isolated nucleic acid of the UC41 gene, useful as marker for
PT diagnosis, prophylaxis and treatment of prostate cancer -

PS Example 1; Page 102; 143pp; English.

XX PCR primers AA63808-09 were used to amplify beta2-microglobulin cDNA
XX sequences, in the course of the invention. The specification
XX describes a human prostate specific protein, designated UC41
XX is a gene that is expressed differentially in prostate cancer
XX compared to non-malignant prostate tissue. It is therefore useful
XX as a prostate cancer marker. Expression of UC41 is upregulated in
XX prostate cancer. UC41 nucleic acids and single-chain antibodies
XX immunospecific for UC41 may be used for detecting prostate cancer
XX cells and therefore for prostate cancer diagnosis.

XX SQ Sequence 28 BP; 10 A; 7 C; 7 G; 4 T; 0 other;

Alignment Scores:

Pred. No.:	Length:
Score: 489	Matches: 28
Percent Similarity: 30.00	Conservative: 5
Best Local Similarity: 87.50%	Mismatches: 2
Query Match: 62.50%	Indels: 1
DB: 21	Gaps: 0

US-10-023-182-6 (1-9) x AA63808 (1-28)

[illegible]

```

Db          19 ATCTTGATGTGGGTGACA 2
RESULT 9
AAL45363
ID AAL45363 standard; DNA; 33 BP.
XX
AC AAL45363;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human acyl CoA synthase 11-77 coding sequence PCR primer #3.
XX
XX Human; acyl CoA synthase 11.77; lipid metabolism disorder; gene therapy;
XX
KW water electrolyte disorder; red blood cell disease; vascular; enzyme;
KW PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN W0200220794-A1.
XX
PD 14-MAR-2002.
XX
PF 29-JUN-2001; 2001WO-CN01083.
XX
PR 30-JUN-2000; 2000CN-0116966.
XX
PA (SHAN-) SHANGHAI BLOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-269632/31.
XX
PT Human acyl CoA Synthetase 11.77 and encoding polynucleotide, used in
PT diagnosis and treatment of lipid metabolism disorders, red blood cell
PT disease and water electrolyte disorders -
XX
PS Example 4; Page 18; 36pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC acyl CoA synthase 11.77. The sequences can be used in the treatment of
CC lipid metabolism disorders, red blood cell disease and water electrolyte
CC disorders. The present sequence is a PCR primer for the coding sequence
CC of the invention.
XX
SQ Sequence 33 BP; 6 A; 4 C; 9 G; 14 T; 0 other;
Alignment Scores:
Pred. No.: 588 Length: 33
Score: 30.00 Matches: 5
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 65.22% Indels: 0
DB: 24 Gaps: 0
US-10-023-182-6 (1-9) x AAL45363 (1-33)
QY 2 LeuSerLeuLeuMetTyrPile 8
Db 13 TTAAGTCCTTTAAGTGTGTG 33
RESULT 10
AAL38296/G
ID AAL38296 standard; DNA; 20 BP.
XX
AC AAL38296;
XX
DT 15-AUG-2002 (first entry)
XX
DE Mouse BH3 interacting domain death mRNA agonist inhibitor SEQ ID 139.
XX
XX Hepatocellular carcinoma; immunomodulatory; cytotoxic; antiinflammatory; hepatitis;
XX
KW haemopoietic; BH3 interacting domain death agonist; liver disease;
KW haematopoietic disorder; developmental disorder; immunological disorder;

```


KM hyperproliferative disorder; apoptosis; mouse; chimeric; 2'-methoxyethyl;
 XX 2'-MOE; phosphorothioate backbone; murine; ds.
 OS Chimeric - Mus musculus.
 XX
 PN WO200220547-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 31-AUG-2001; 2001WO-US27316.
 XX
 PR 07-SEP-2000; 2000US-0657346.
 XX
 PR 07-MAR-2001; 2001US-0800631.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Zhang H, Wyatt JR;
 XX
 DR WPI; 2002-339386/42.
 XX
 PT Novel antisense compound targeted to nucleic acid molecule encoding the
 PT BH3 interacting domain death agonist, useful for treating animals with
 PT diseases associated with BH3 interacting domain death agonist, e.g.
 PT hepatitis
 XX
 PS Claim 3; Page 90; 17pp; English.
 XX
 CC The invention relates to a compound 8 to 50 nucleotides in length
 CC targeted to a nucleic acid molecule encoding a BH3 interacting domain
 CC death agonist, where the compound specifically hybridizes with and
 CC inhibits the expression of the BH3 interacting domain death agonist. The
 CC compound of the invention is useful for inhibiting the expression of the
 CC BH3 interacting domain death agonist in cells or tissues. The compound is
 CC also useful for treating an animal having a disease or condition
 CC associated with the BH3 interacting domain death agonist, e.g.
 CC hematopoietic disorder, hyperproliferative disorder, a developmental
 CC disorder, immunological disorder, or a disease or condition of the liver
 CC e.g., hepatitis, or a condition associated with apoptosis. The compound
 CC is useful for diagnostics, therapeutics, prophylaxis and as research
 CC reagents and kits. This polynucleotide sequence represents an antisense
 CC oligonucleotide inhibitor of the DNA from mouse BH3 interacting domain
 CC death agonist RNA of the invention.
 CC NOTE: This sequence is a chimeric oligonucleotide 20 nucleotides in
 CC length, which is flanked on both sides by five-nucleotide 'wings'. The
 CC wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The
 CC internucleoside (backbone) linkages are phosphorothioate (P-S) throughout
 CC the oligonucleotide.
 XX
 SQ Sequence 20 BP; 8 A; 5 C; 6 G; 1 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 515 Length: 20
 Score: 29.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 83.33% Mismatches: 0
 Query Match: 63.04% Indels: 0
 DB: 24 Gaps: 0
 US-10-023-182-6 (1-9) x AA138296 (1-20)
 QY 2 LeuSerLeuMetTrp 7
 ID AAD00156/c
 XX AAD00156 standard; DNA; 21 BP.
 AC AAD00156;
 XX
 DT 31-JUL-2000 (first entry)
 XX
 DE Reverse PCR primer R2, for construction of PCR-464 vector.

XX
 XX CAMEL, CTL-recognised Antigen on MELanoma; cytotoxic T lymphocyte; CTL;
 XX tumour-associated antigen; LAGE-1; NY-ESO-1; anticancer; melanoma; human;
 XX cancer; immunotherapy; immune response; PCR primer; ss.
 OS Homo sapiens.
 XX
 PN WO200023584-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 15-OCT-1999; 99WO-EP07832.
 XX
 PR 16-OCT-1998; 98EP-0119583.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX (URHO-) UNIV HOSPITAL LEIDEN.
 XX
 PI Schrier PI, Aarnoudse CA, Heider K, Klade C;
 XX
 DR WPI; 2000-339685/29.
 XX
 PT Tumor-associated antigen useful for cancer immunotherapy is encoded by
 PT the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA -
 XX
 PS Disclosure; Page 66; 73pp; English.
 XX
 CC The present DNA sequence is the reverse PCR primer R2, used along with
 CC forward PCR primer SpEF-PSV, to generate the deletion construct,
 CC PCR-464 of CAMEL cDNA clone 4H8.
 CC The tumour-associated antigen, CAMEL (Cytotoxic T lymphocytes (CTL)-
 CC recognised Antigen on MELanoma) is encoded by the open reading frame
 CC (ORF)-1 of LAGE-1 gene, a tumour-specific antigen. It shows strong
 CC homology with NY-ESO-1, a tumour-specific antigen. The tumour-associated
 CC antigen displayed on melanoma cells is recognised by cytotoxic T
 CC lymphocytes. CAMEL is expressed in tumour cell lines, tumour tissues
 CC (e.g. breast and lung) and in restricted number of healthy tissues. It
 CC has anticancer activity. CAMEL, tumour antigen and immunogenic peptides
 CC derived from it are useful for cancer immunotherapy. They have the
 CC potential to induce an immune response, by eliciting a CTL response. The
 CC DNA molecule is used for construction of recombinant or fusion proteins.
 XX
 SQ Sequence 21 BP; 6 A; 7 C; 4 G; 4 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 544 Length: 21
 Score: 29.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 63.04% Indels: 0
 DB: 21 Gaps: 0
 US-10-023-182-6 (1-9) x AAD00156 (1-21)
 QY 5 LeuMetTrpLeuThr 9
 ID AA169858/c
 XX AA169858 standard; DNA; 30 BP.
 AC AA169858;
 XX
 DT 02-JAN-2002 (first entry)
 XX
 DE SV40 large T antigen nuclear localisation peptide coding sequence.
 XX
 XX SV40; simian virus 40; large T antigen; capsid; virus-like particle;
 KM nuclear localisation signal; VP3; ds.
 XX
 OS Rhesus macaque polyoma virus.
 XX

PM JP2001169777-A.
XX
XX 26-JUN-2001.
XX
XX 30-JUL-1999; 99JP-0249140.
XX PF
XX 30-JUL-1999; 99JP-0249140.
XX PR
XX (HAND/) HANDA H.
XX
XX WPI; 2001-599854/68.
XX
XX New virus-like particles from VP3 capsid protein of adeno-associated
XX virus, comprise a peptide containing a nucleus-shifting signal
XX connected to its N-terminal -
XX
XX
XX Disclosure; Page 22; 33pp; Japanese.
XX
XX The present sequence is provided in a specification relating to a
XX virus-like particle-forming protein, and to a peptide containing a
XX nuclear-shifting signal at its N-terminus that can form virus-like
XX particles by shifting to the nucleus of the animal cell in which it
XX is expressed. The method is used for forming virus-like particles
XX from the VP3 capsid protein of adeno-associated virus (AAV).
XX
SQ Sequence 30 BP; 13 A; 6 C; 8 G; 3 T; 0 other;

Alignment Scores:
Pred. No.: 810 Length: 30
Score: 29.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 63.04% Indels: 0
DB: 22 Gaps: 0

US-10-023-182-6 (1-9) x AAI69858 (1-30)

QY 2 LeuSerLeuMetTrp 7
DB 27 CTTTCGCTTCTTCTTGG 10

RESULT 13
ABX70076
ID ABX70076 standard; DNA; 30 BP.
XX
XX ABX70076;
XX
XX 07-MAY-2003 (first entry)
XX
XX Novel Helicobacter pylori gene PCR primer #3047.
XX
XX Protein-protein interaction; ulcer; selected interacting domain;
XX SID; PCR; primer; ss.
XX
XX Helicobacter pylori.
XX
XX WO200266501-A2.
XX
XX 29-AUG-2002.
XX
XX 28-DEC-2001; 2001WO-EP15428.
XX PF
XX 02-JAN-2001; 2001US-259302P.
XX PR
XX (HYBR-) HYBRIGENICS.
XX PA
XX (INSP) INST PASTER.
XX
XX Legrain P, Rain J, Colland F, De Reuse H, Labigne A;
XX WPI; 2002-674910/72.
XX
XX New complexes of protein-protein interactions in Helicobacter pylori,
XX useful for identifying modulating compounds for treating or preventing

PT ulcers in mammals -
XX
XX Example 9; Page 583; 642pp; English.
XX
XX The invention describes a complex of protein-protein interactions in
XX Helicobacter pylori selected from 421 complexes given in the
XX specification. The complex of protein-protein interactions are useful
XX for screening for agents which modulate the interaction of proteins.
XX Modulating compounds which binds to a targeted bacterial protein may be
XX used for treating or preventing ulcers in a human or animal. This
XX sequence represents a primer used to isolate polynucleotides encoding
XX Helicobacter pylori proteins for studies on protein-protein
XX interactions.
XX
SQ Sequence 30 BP; 11 A; 8 C; 5 G; 3 T; 3 U; 0 other;

Alignment Scores:
Pred. No.: 810 Length: 30
Score: 29.00 Matches: 4
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 63.04% Indels: 0
DB: 24 Gaps: 0

US-10-023-182-6 (1-9) x ABX70076 (1-30)

QY 4 LeuLeuMetTrpIleThr 9
DB 5 AUCAGATGTGATCACC 22

RESULT 14
AAT77768/C
ID AAT77768 standard; CDNA; 31 BP.
XX
XX AAT77768;
XX
XX 30-SEP-1997 (first entry)
XX
XX SV40 T antigen nuclear localisation signal amplification primer #1.
XX
XX SH2 binding domain; LexA-FcERI-gamma-C₁; reporter yeast; RBL-2H3 cell;
XX Fc-epsilon-RI; detection; protein-protein interaction; phosphorylation;
XX tyrosine; signal transduction pathway; activated cell-surface receptor;
XX post-translationally modified protein; mast cell activation; PCR;
XX amplify; polymerase chain reaction; primer; ss.
XX
XX Synthetic.
XX
XX US5637463-A.
XX
XX 10-JUN-1997.
XX PD
XX 04-MAY-1995; 95US-0434730.
XX PF
XX 04-MAY-1995; 95US-0434730.
XX PR
XX (HOFF) HOFFMANN LA ROCHE INC.
XX
XX Dalton S, Kochan JP, Osborne NA;
XX WPI; 1997-319067/29.
XX
XX Detection of protein-protein interactions - dependent on
XX post-translational modification of one of the protein, also new cDNA
XX and protein molecules containing SH2 domains
XX
XX Example; Column 9; 30pp; English.
XX
XX The sequences given in AAT77766-69 are primers which were used in the
XX amplification of binding protein coding sequences for use in the method
XX of the invention for detecting an interaction between a first test
XX protein and a second test protein. The method may be used for detecting
XX protein-protein interactions requiring specific post-translational

CC modifications, e.g. the phosphorylation of tyrosine residues, which is
 CC a critical step in the signal transduction pathways of activated cell-
 CC surface receptors. It may also be used for identifying amino acid
 CC residues that are critical for protein-protein interactions to occur
 CC and for identifying novel proteins that bind to post-translationally
 CC modified proteins. The method may be used for identifying proteins
 CC that can post-translationally modify, or be modified by, other proteins
 CC and for identifying molecules that inhibit protein-protein interactions.
 CC The novel SH2 proteins may be used in screening inhibitors of mast cell
 CC activation.

CC SQ Sequence 31 BP, 12 A, 6 C, 12 G, 1 T, 0 other;

Alignment Scores:
 Pred. No.: 840 Length: 31
 Score: 29.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 83.33% Mismatches: 0
 Query Match: 63.04% Indels: 0
 DB: 18 Gaps: 0

US-10-023-182-6 (1-9) X AAT77766 (1-31)

OY 2 LeuSerLeuMetTTP 7
 DB 25 CTTTCTCTCTCTTTGG 8

RESULT 15

AAT77769
 ID AAT77769 standard; cDNA; 31 BP.

AC AAT77769;

DT 30-SEP-1997 (first entry)

DE SV40 T antigen nuclear localization signal amplification primer #2.

XX SH2 binding domain; LexA-FcERI-gamma-CT; reporter Yeast; RBL-2H3 cell;
 XX Fc-epsilon-R1; detection; protein-protein interaction; phosphorylation;
 XX tyrosine; signal transduction pathway; activated cell-surface receptor;
 XX post-translational modified protein; mast cell activation; PCR;
 XX amplify; polymerase chain reaction; primer; ss.

OS Synthetic.

XX US5637463-A.

XX 10-JUN-1997.

XX 04-MAY-1995; 95US-0434730.

XX 04-MAY-1995; 95US-0434730.

XX (HOFF) HOFFMANN LA ROCHE INC.

XX Dalton S, Kochan JP, Osborne MA;

XX WPI; 1997-319067/29.

PT Detection of protein-protein interactions - dependent on
 PT post-translational modification of one of the protein, also new cDNA
 PT and protein molecules containing SH2 domains

PS Example; Column 9; 30pp; English.

XX The sequences given in AAT77766-69 are primers which were used in the
 CC amplification of binding protein coding sequences for use in the method
 CC of the invention for detecting an interaction between a first test
 CC protein and a second test protein. The method may be used for detecting
 CC protein-protein interactions requiring specific post-translational
 CC modifications, e.g. the phosphorylation of tyrosine residues, which is
 CC a critical step in the signal transduction pathways of activated cell-
 CC surface receptors. It may also be used for identifying amino acid

CC residues that are critical for protein-protein interactions to occur
 CC and for identifying novel proteins that bind to post-translationally
 CC modified proteins. The method may be used for identifying proteins
 CC that can post-translationally modify, or be modified by, other proteins
 CC and for identifying molecules that inhibit protein-protein interactions.
 CC The novel SH2 proteins may be used in screening inhibitors of mast cell
 CC activation.

CC SQ Sequence 31 BP, 3 A, 10 C, 4 G, 14 T, 0 other;

Alignment Scores:
 Pred. No.: 840 Length: 31
 Score: 29.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 83.33% Mismatches: 0
 Query Match: 63.04% Indels: 0
 DB: 18 Gaps: 0

US-10-023-182-6 (1-9) X AAT77769 (1-31)

OY 2 LeuSerLeuMetTTP 7
 DB 11 CTTTCTCTCTCTTTGG 28

Search completed: February 21, 2004, 19:51:59
 Job time : 172 secs

Mon Feb 23 07:48:08 2004

US-10-023-182-6.rml

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: February 21, 2004, 19:28:16 ; Search time 39.4138 Seconds
(without alignments)
100.788 Million cell updates/sec

Title: US-10-023-182-6
Perfect score: 46
Sequence: 1 QUSLIMWT 9

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 segs, 220691566 residues

Total number of hits satisfying chosen parameters: 583842

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame.p2n.model -DEV=rlh
-Q=/cgn2_1/USPTO.spool/US1002182/runat.20022004.111043.21349/app.query.fasta.1.597
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rm1 -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFM=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=33
-USER=US1002182.eccn.1.1.95@runat.20022004.111043.21349 -NCPU=6 -ICPU=3
-NO_MAP_LARGEOUTERY -NEG_COPIES=0 -WAT -DSFLOCK=100 -LONGIOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/prodata/1/ina/5A_COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/prodata/1/ina/PTUS_COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfillseq1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	69.6	19	1	US-08-791-495-3	Sequence 3, Appl1
C 2	67.4	27	2	US-09-122-230-13	Sequence 13, Appl1
C 3	67.4	33	1	US-08-463-224-61	Sequence 61, Appl1
C 4	67.4	33	2	US-08-463-377-61	Sequence 61, Appl1
C 5	65.2	28	3	US-08-348-548-24	Sequence 24, Appl1
C 6	65.2	28	4	US-09-579-236-12	Sequence 12, Appl1
C 7	65.2	28	5	PCT-US95-15716-24	Sequence 24, Appl1
C 8	65.2	31	3	US-09-358-683-4	Sequence 4, Appl1
C 9	63.0	20	4	US-09-657-346A-139	Sequence 139, Appl1
C 10	63.0	31	1	US-08-434-730-3	Sequence 3, Appl1
C 11	63.0	31	1	US-08-434-730-4	Sequence 4, Appl1
C 12	60.9	18	1	US-08-284-860A-5	Sequence 5, Appl1

C 13	60.9	28	18	1	US-08-318-867A-3	Sequence 3, Appl1
C 14	60.9	28	18	3	US-08-430-277A-3	Sequence 9, Appl1
C 15	60.9	28	20	2	US-08-775-009-9	Sequence 22, Appl1
C 16	60.9	28	20	3	US-09-358-683-22	Sequence 6817, Ap
C 17	60.9	28	20	4	US-09-422-978-6817	Sequence 4778, Ap
C 18	60.9	27	20	4	US-09-198-452A-4778	Sequence 4, Appl1
C 19	58.7	27	21	3	US-08-952-376-4	Sequence 4, Appl1
C 20	58.7	27	23	2	US-08-460-890A-4	Sequence 4, Appl1
C 21	58.7	27	23	3	US-08-167-641C-4	Sequence 4, Appl1
C 22	58.7	27	23	3	US-08-460-971A-4	Sequence 4, Appl1
C 23	58.7	27	23	3	US-08-462-040-4	Sequence 4, Appl1
C 24	58.7	27	23	4	US-09-306-420C-7	Sequence 7, Appl1
C 25	58.7	27	24	2	US-09-128-312-3	Sequence 3, Appl1
C 26	58.7	27	24	4	US-09-128-312-4	Sequence 4, Appl1
C 27	58.7	27	24	4	US-09-370-683-3	Sequence 3, Appl1
C 28	58.7	27	24	4	US-09-370-683-4	Sequence 4, Appl1
C 29	58.7	27	26	2	US-08-859-898-1271	Sequence 1271, Ap
C 30	58.7	27	26	4	US-09-225-928-1271	Sequence 13, Appl1
C 31	58.7	27	26	4	US-09-560-419-13	Sequence 1271, Ap
C 32	58.7	27	26	4	US-09-225-201B-1271	Sequence 22, Appl1
C 33	58.7	27	30	1	US-08-387-315A-22	Sequence 22, Appl1
C 34	58.7	27	30	2	US-08-754-559-22	Sequence 53, Appl1
C 35	56.5	26	20	3	US-09-484-345-53	Sequence 2, Appl1
C 36	56.5	26	24	2	US-08-739-401A-2	Sequence 28, Appl1
C 37	56.5	26	24	4	US-09-502-653-28	Sequence 97, Appl1
C 38	56.5	26	28	4	US-09-360-545-97	Sequence 16, Appl1
C 39	56.5	26	29	3	US-08-617-454-16	Sequence 7, Appl1
C 40	56.5	26	29	3	US-08-848-760B-7	Sequence 29, Appl1
C 41	56.5	26	31	2	US-08-629-001A-29	Sequence 108, Appl1
C 42	56.5	26	31	3	US-08-642-274D-108	Sequence 80, Appl1
C 43	56.5	26	33	2	US-08-378-617A-15	Sequence 158, Appl1
C 44	56.5	26	33	3	US-09-295-028-80	
C 45	54.3	25	17	3	US-08-985-162-158	

ALIGNMENTS

RESULT 1
US-08-791-495-3/c
; Sequence 3, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Ieth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godetaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: L1-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-791-495-3

Alignment Scores:
Pred. No.: 27.5 Length: 19
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.57% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-6 (1-9) x US-08-791-495-3 (1-19)

QY 3 SerLeuLeuMetTTPile 8
DB 18 TCCTCTGTGATGTGATC 1

RESULT 2
US-09-122-230-13
Sequence 13, Application US/09122230A
Patent No. 5973228
GENERAL INFORMATION:
APPLICANT: Carlson, et al.
TITLE OF INVENTION: Coniferin Beta Glucosidase cDNA for Modifying Lignin
FILE REFERENCE: 50532
CURRENT APPLICATION NUMBER: US/09/122,230A
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: U.S. 60/053,566
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 13
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer for the
US-09-122-230-13

Alignment Scores:
Pred. No.: 62.7 Length: 27
Score: 31.00 Matches: 4
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 0
Query Match: 67.39% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-6 (1-9) x US-09-122-230-13 (1-27)

QY 1 GinLeuSerLeuLeuMetTTPile 8
DB 4 GAGTGTCTGTGTGATGTGAGTA 27

RESULT 3
US-08-463-224-61/C
Sequence 61, Application US/08463224
Patent No. 5807824
GENERAL INFORMATION:
APPLICANT: van Oostrum, Jan
APPLICANT: Boyar, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert

APPLICANT: van Heeke, Gino
TITLE OF INVENTION: C5a Receptor Antagonists Having
Substantially No. 5807824agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Wentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,224
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-224-61

Alignment Scores:
Pred. No.: 78.4 Length: 33
Score: 31.00 Matches: 5
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 67.39% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-6 (1-9) x US-08-463-224-61 (1-33)

QY 2 LeuSerLeuLeuMetTTPile 8
DB 28 TTGAGCCTCATGTCTGTGATC 8

RESULT 4
US-08-463-377-61/C
Sequence 61, Application US/08463377
Patent No. 5837499
GENERAL INFORMATION:
APPLICANT: van Oostrum, Jan
APPLICANT: Boyar, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: van Heeke, Gino
TITLE OF INVENTION: C5a Receptor Antagonists Having
Substantially No. 5837499agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Wentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,377
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-377-61

Alignment Scores:
Pred. No.: 78.4 Length: 33
Score: 31.00 Matches: 5
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 67.39% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-6 (1-9) x US-08-463-377-61 (1-33)
QY 2 LeuSerLeuMetTrpIleThr 8
Db 28 TTGAGCTCATGCTGCTGATC 8

RESULT 5
US-08-348-548-24/c
Sequence 24, Application US/08348548
Patent No. 6258529
GENERAL INFORMATION:
APPLICANT: Berdoz, Jose
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-348-548-24

Alignment Scores:
Pred. No.: 100 Length: 28
Score: 30.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 65.22% Indels: 0
DB: 3 Gaps: 0

US-10-023-182-6 (1-9) x US-08-348-548-24 (1-28)
QY 2 LeuSerLeuMetTrpIleThr 9
Db 27 ATGTCCCTGCTGCTGCTGATGACG 4

RESULT 6
US-09-579-236-12/c
Sequence 12, Application US/09579236
Patent No. 6369195
GENERAL INFORMATION:
APPLICANT: VETTRI, ROBERT
TITLE OF INVENTION: A NOVEL, PROSTATE-SPECIFIC GENE FOR DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE CANCER
FILE REFERENCE: USOC:024
CURRENT APPLICATION NUMBER: US/09/579,236
CURRENT FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 09/247,188
PRIOR FILING DATE: 1999-02-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 28
TYPE: DNA
ORGANISM: Homo sapiens
US-09-579-236-12

Alignment Scores:
Pred. No.: 100 Length: 28
Score: 30.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 65.22% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-6 (1-9) x US-09-579-236-12 (1-28)
QY 2 LeuSerLeuMetTrpIleThr 9
Db 26 CTTTCATTCCTGCTGATGACG 3

RESULT 7
PCT-US95-15716-24/c
Sequence 24, Application PC/TUS9515716
GENERAL INFORMATION:
APPLICANT: Berdoz, Jose
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.308
CURRENT APPLICATION DATA:

```
/ APPLICATION NUMBER: PCT/US95/15716
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/348,548
/ FILING DATE: 01-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 06132/009001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-5070
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
PCT-US95-15716-24

Alignment Scores:
Pred. No.: 100 Length: 28
Score: 30.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 65.22% Indels: 0
DB: 5 Gaps: 0

US-10-023-182-6 (1-9) x PCT-US95-15716-24 (1-28)
Qy 2 LeuSerLeuMetTrrPleThr 9
Db 27 ATGTCCTCGCTGCTGTGTCGACG 4

RESULT 8
US-09-358-683-4/c
/ Sequence 4, Application US/09358683
/ Patent No. 6200807
/ GENERAL INFORMATION:
/ APPLICANT: C. Frank Bennett
/ TITLE OF INVENTION: ANTISENSE MODULATION OF SHP-2 EXPRESSION
/ FILE REFERENCE: R1S-0082
/ CURRENT APPLICATION NUMBER: US/09/358,683
/ CURRENT FILING DATE: 1999-07-21
/ NUMBER OF SEQ ID NOS: 47
/ SEQ ID NO 4
/ LENGTH: 31
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: PCR Probe
US-09-358-683-4

Alignment Scores:
Pred. No.: 112 Length: 31
Score: 30.00 Matches: 4
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 65.22% Indels: 0
DB: 3 Gaps: 0

US-10-023-182-6 (1-9) x US-09-358-683-4 (1-31)
Qy 4 LeuLeuMetTrrPleThr 9
Db 19 ATCTTGATGTGGTGACA 2

RESULT 9
US-09-657-346A-139/c
/ Sequence 139, Application US/09657346A

Patent No. 6503754
/ GENERAL INFORMATION:
/ APPLICANT: Hong Zhang
/ TITLE OF INVENTION: ANTISENSE MODULATION OF B33 INTERACTING DOMAIN DEATH AGONIST
/ FILE REFERENCE: R1S-0135
/ CURRENT APPLICATION NUMBER: US/09/657,346A
/ CURRENT FILING DATE: 2000-03-07
/ NUMBER OF SEQ ID NOS: 174
/ SEQ ID NO 139
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense oligonucleotide
US-09-657-346A-139

Alignment Scores:
Pred. No.: 106 Length: 20
Score: 29.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 63.04% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-6 (1-9) x US-09-657-346A-139 (1-20)
Qy 2 LeuSerLeuMetTrrP 7
Db 20 CTCAGCTTCTCTGTGG 3

RESULT 10
US-08-434-730-3/c
/ Sequence 3, Application US/08434730
/ Patent No. 5637463
/ GENERAL INFORMATION:
/ APPLICANT: Dalton, Stephen
/ APPLICANT: Kochan, Jarema P
/ TITLE OF INVENTION: METHOD TO DETECT PROTEIN-PROTEIN INTERACTIONS
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hoffmann-La Roche Inc
/ STREET: 340 Kingsland Street
/ CITY: Nutley
/ STATE: NJ
/ COUNTRY: USA
/ ZIP: 07110
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/434,730
/ FILING DATE: 04-MAY-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Semionow, Raina
/ REGISTRATION NUMBER: 39022
/ REFERENCE/DOCKET NUMBER: 9069
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (201)235-4391
/ TELEFAX: (201)235-2363
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 31 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
```

HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-434-730-3

Alignment Scores:

Pred. No.:	173	Length:	31
Score:	29.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	83.33%	Mismatches:	0
Query Match:	63.04%	Indels:	0
DB:	1	Gaps:	0

US-10-023-182-6 (1-9) x US-08-434-730-3 (1-31)

QY 2 LeuSerleuMetTrp 7
Db 25 CTTCTCTCTCTCTTGG 8

RESULT 11

US-08-434-730-4
Sequence 4, Application US/08434730
Patent No. 5637463
GENERAL INFORMATION:
APPLICANT: Dalton, Stephen
APPLICANT: Kochan, Jarema P
TITLE OF INVENTION: METHOD TO DETECT PROTEIN-PROTEIN
INTERACTIONS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,730
FILING DATE: 04-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Semlow, Ralua
REGISTRATION NUMBER: 39022
REFERENCE/DOCKET NUMBER: 9069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)235-4391
TELEFAX: (201)235-2363
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-434-730-4

Alignment Scores:

Pred. No.:	173	Length:	31
Score:	29.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	83.33%	Mismatches:	0
Query Match:	63.04%	Indels:	0
DB:	1	Gaps:	0

US-10-023-182-6 (1-9) x US-08-434-730-4 (1-31)

QY 2 LeuSerleuMetTrp 7
Db 11 CTTCTCTCTCTCTTGG 28

RESULT 12

US-08-284-860A-5/C
Sequence 5, Application US/08284860A
Patent No. 5643762
GENERAL INFORMATION:
APPLICANT: Oshima, Atsushi
APPLICANT: Inouye, Sumiko
APPLICANT: Inouye, Masayori
TITLE OF INVENTION: METHOD FOR SYNTHESIZING SINGLE-STRANDED
STEM-LOOP DNA, THE PRODUCTS AND USES THEREFOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates, P.C.
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,860A
FILING DATE: 02-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377,5577P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
TELEX: 834809
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-284-860A-5

Alignment Scores:

Pred. No.:	145	Length:	18
Score:	28.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	66.67%	Mismatches:	0
Query Match:	60.87%	Indels:	0
DB:	1	Gaps:	0

US-10-023-182-6 (1-9) x US-08-284-860A-5 (1-18)

QY 4 LeuMetTrpIleThr 9
Db 18 CTGATTCGTGATTAAC 1

RESULT 13

US-08-318-867A-3/C
Sequence 3, Application US/08318867A
Patent No. 5714323
GENERAL INFORMATION:
APPLICANT: ATUSHI OSHIMA
APPLICANT: SUMIKO INOUE
APPLICANT: MASAYORI INOUE
TITLE OF INVENTION: OVER EXPRESSION OF SINGLE-STRANDED
MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:

ADDRESSEE: WEISER & ASSOCIATES, P.C.
STREET: 230 S. 15th ST.
CITY: PHILADELPHIA, PA
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,867A
FILING DATE: MAY 4, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GERARD J. WEISER
REFERENCE/DOCKET NUMBER: 377.6120P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 875-8383
TELEFAX: (215) 875-8394
INFORMATION FOR SEQ. ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-318-867A-3

Alignment Scores:
Pred. No.: 145
Score: 28.00
Percent Similarity: 100.00%
Best Local Similarity: 66.67%
Query Match: 60.87%
DB: 1
Gaps: 0

US-10-023-182-6 (1-9) x US-08-318-867A-3 (1-18)

QY 4 LeuLeuMeCTTp1eThr 9
DB 18 CTGATTCGTGTGATTAACC 1

RESULT 14
US-08-430-277A-3/C
Sequence 3, Application US/08430277A
Patent No. 6043028
GENERAL INFORMATION:
APPLICANT: Onshima, Atsushi
APPLICANT: Inouye, Masayori
APPLICANT: Inouye, Sumiko
TITLE OF INVENTION: METHOD FOR SYNTHESIZING SINGLE-STRANDED
TITLE OF INVENTION: STEM-LOOP DNAs, THE PRODUCTS AND USES THEREFORE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,277A
FILING DATE: 28-APR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 913(377).5820

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ. ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-430-277A-3

Alignment Scores:
Pred. No.: 145
Score: 28.00
Percent Similarity: 100.00%
Best Local Similarity: 66.67%
Query Match: 60.87%
DB: 3
Gaps: 0

US-10-023-182-6 (1-9) x US-08-430-277A-3 (1-18)

QY 4 LeuLeuMeCTTp1eThr 9
DB 18 CTGATTCGTGTGATTAACC 1

RESULT 15
US-08-775-009-9
Sequence 9, Application US/08775009
Patent No. 5935783
GENERAL INFORMATION:
APPLICANT: Gong, Wellong
APPLICANT: Emanuel, Beverly S.
APPLICANT: Budarf, Marcia L.
APPLICANT: Roe, Bruce
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digestion and
TITLE OF INVENTION: Velocardiofacial Syndrome Minimal Critical Region
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSER: No. 5915783rls, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ. ID NO.: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-775-009-9

Alignment Scores:
Pred. No.: 163
Length: 20

Score: 28.00
 Percent Similarity: 100.00%
 Best Local Similarity: 80.00%
 Query Match: 60.87%
 DB: 2
 Matches: 4
 Conservative: 1
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-10-023-182-6 (1-9) x US-08-775-009-9 (1-20)

QY 5 LeuMetTrpIleThr 9
 |||||
 Db 5 CTGATGGGTAAACA 19

Search completed: February 21, 2004, 22:53:55
 Job time : 40.4138 secs

Mon Feb 23 07:48:08 2004

us-10-023-182-6.rmpb

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2004, 21:41:37 ; Search time 216.931 Seconds
(without alignments)
152.826 Million cell updates/sec

Title: US-10-023-182-6
Perfect score: 46
Sequence: 1 QLSILMWIT 9

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Delop 6.0, Delext 7.0

Searched: 2449703 seqs, 1841816367 residues
Total number of hits satisfying chosen parameters: 1147742

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1h
-O=/cgn2_1/USPTO.spool/US10023182/rnat 20022004_11045_21435/app.query.fasta_1.597
-DB=Published Applications NA -OPMT=fastap -SUFFIX=rmpb -MINMATCH=0.1
-LOOPCT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonsum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MATEL=33 -USER=US10023182 @CEN_1_1_560 @rnat 20022004_11045_21435 -NCPU=6
-ICPU=3 -NO MMAP -LARGEOVERLY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA: *
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq: *
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq: *
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq: *
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq: *
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq: *
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq: *
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq: *
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq: *
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq: *
10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq: *
11: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq: *
12: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq: *
13: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq: *
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq: *
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq: *
16: /cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq: *
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq: *
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query *
No. Score Match Length DB ID Description

1	34	73.9	25	15	US-10-098-263B-89291	Sequence 89291, A
2	34	73.9	25	15	US-10-098-263B-89292	Sequence 89292, A
3	31	67.4	24	10	US-09-953-343-1	Sequence 1, Appl
4	31	67.4	24	11	US-09-953-344-1	Sequence 12, Appl
5	30	65.2	28	9	US-09-800-631-139	Sequence 139, App
6	29	63.0	20	12	US-10-388-263-791	Sequence 791, App
7	29	63.0	20	16	US-10-293-783-139	Sequence 139, App
8	29	63.0	25	15	US-10-098-263B-1045	Sequence 1045, A
9	29	63.0	25	15	US-10-098-263B-27820	Sequence 27820, A
10	28	60.9	20	12	US-10-349-143-6817	Sequence 6817, Ap
11	28	60.9	22	9	US-09-930-218-14	Sequence 14, Appl
12	28	60.9	22	13	US-10-431-338-14	Sequence 14, Appl
13	28	60.9	23	10	US-09-957-667-7	Sequence 7, Appl
14	28	60.9	25	15	US-10-098-263B-60841	Sequence 60841, A
15	28	60.9	26	12	US-09-981-565A-187	Sequence 187, App
16	28	60.9	26	12	US-09-930-512-81	Sequence 81, Appl
17	28	60.9	29	13	US-10-181-157-18	Sequence 18, Appl
18	28	60.9	29	13	US-10-357-043-26	Sequence 26, Appl
19	28	60.9	20	12	US-10-289-762-4778	Sequence 4778, Ap
20	27	58.7	21	9	US-09-968-355-12	Sequence 12, Appl
21	27	58.7	21	13	US-10-363-798-10	Sequence 10, Appl
22	27	58.7	23	11	US-09-781-891D-1	Sequence 1, Appl
23	27	58.7	23	15	US-10-260-451-7	Sequence 7, Appl
24	27	58.7	23	15	US-10-263-872-26	Sequence 26, Appl
25	27	58.7	25	13	US-10-027-632-177797	Sequence 177797, A
26	27	58.7	25	14	US-10-027-632-177797	Sequence 177797, A
27	27	58.7	25	15	US-10-098-263B-11757	Sequence 11757, A
28	27	58.7	27	15	US-09-804-582-1173	Sequence 173, App
29	27	58.7	28	12	US-10-310-740-5	Sequence 5, Appl
30	27	58.7	30	15	US-10-085-906-92	Sequence 92, Appl
31	27	58.7	17	15	US-10-156-306-4956	Sequence 4956, Ap
32	26	56.5	21	9	US-09-765-081-303	Sequence 303, App
33	26	56.5	21	9	US-09-921-992-77	Sequence 77, Appl
34	26	56.5	21	12	US-10-277-116-333	Sequence 33, App
35	26	56.5	24	11	US-09-798-733A-23	Sequence 23, Appl
36	26	56.5	24	11	US-09-883-152-33	Sequence 33, Appl
37	26	56.5	25	11	US-09-940-185-1153	Sequence 1153, App
38	26	56.5	25	15	US-10-098-263B-1046	Sequence 1046, Ap
39	26	56.5	25	15	US-10-098-263B-1915	Sequence 1915, Ap
40	26	56.5	25	15	US-10-098-263B-10188	Sequence 10188, A
41	26	56.5	25	15	US-10-098-263B-14220	Sequence 14220, A
42	26	56.5	25	15	US-10-098-263B-16235	Sequence 16235, A
43	26	56.5	25	15	US-10-098-263B-16236	Sequence 16236, A
44	26	56.5	25	15	US-10-098-263B-17017	Sequence 17017, A
45	26	56.5	25	15	US-10-098-263B-17017	Sequence 17017, A

ALIGNMENTS

RESULT 1
US-10-098-263B-89291
Sequence 89291, Appl
Publication No. US20030104410A1
GENERAL INFORMATION:
Applicant: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 89291
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-89291
ALIGNMENT Scores:
Pred. No.: 76.9
Score: 34.00
Percent Similarity: 87.50%
Length: 25
Matches: 6
Conservative: 1

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
665	29.00	85.71%	57.14%	63.04%	25	4	2	1	0	0

US-10-023-182-6 (1-9) x US-10-098-263B-1045 (1-25)

QY 3 SerLeuLeuMetTyrIleThr 9

DB 22 AGTACTATCATGTGGGTACG 2

RESULT 10

US-10-098-263B-27820

Sequence 27820, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Miltman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 60/276,759

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO: 27820

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-098-263B-27820

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
665	29.00	100.00%	83.33%	63.04%	25	5	1	0	0	0

US-10-023-182-6 (1-9) x US-10-098-263B-27820 (1-25)

QY 2 LeuSerLeuLeuMetTyr 7

DB 3 CTCAGTCTCTGTGTGG 20

RESULT 11

US-10-349-143-6817

Sequence 6817, Application US/10349143

Publication No. US20040005584A1

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CPL

CURRENT APPLICATION NUMBER: US/10/349,143

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/09/422,978

PRIOR FILING DATE: 1999-10-20

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO: 6817

LENGTH: 20

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: primer_bind

LOCATION: 1..20

OTHER INFORMATION: upstream amplification primer 99-19584 for SEQ 2883,

US-10-349-143-6817

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
807	28.00	100.00%	83.33%	60.87%	20	5	1	0	0	0

US-10-023-182-6 (1-9) x US-10-349-143-6817 (1-20)

QY 2 LeuSerLeuLeuMetTyr 7

DB 2 TTATCACTATGTGGTTGG 19

RESULT 12

US-09-930-218-14/C

Sequence 14, Application US/09930218

Patent No. US20020034810A1

GENERAL INFORMATION:

APPLICANT: goldshmidt, orit

APPLICANT: pecker, itis

APPLICANT: vlodavsky, israel

APPLICANT: israel, michael

TITLE OF INVENTION: AVIAN AND REPTILE DERIVED POLYNUCLEOTIDE ENCODING A POLYPEPTIDE H

FILE REFERENCE: 01/22335

CURRENT APPLICATION NUMBER: US/09/930,218

CURRENT FILING DATE: 2001-08-16

PRIOR APPLICATION NUMBER: 09/666,390

PRIOR FILING DATE: 2000-09-20

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 14

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: synthetic polynucleotide

US-09-930-218-14

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
893	28.00	100.00%	100.00%	60.87%	22	5	0	0	0	0

US-10-023-182-6 (1-9) x US-09-930-218-14 (1-22)

QY 3 SerLeuLeuMetTyr 7

DB 15 TCCCTCTCGATGTGG 1

RESULT 13

US-10-431-438-14/C

Sequence 14, Application US/10431438

Publication No. US20030180788A1

GENERAL INFORMATION:

APPLICANT: goldshmidt, orit

APPLICANT: pecker, itis

APPLICANT: vlodavsky, israel

APPLICANT: israel, michael

TITLE OF INVENTION: AVIAN AND REPTILE DERIVED POLYNUCLEOTIDE ENCODING A POLYPEPTIDE H

FILE REFERENCE: 26013

```
; CURRENT APPLICATION NUMBER: US/10/431,438
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide
US-10-431-438-14

Alignment Scores:
Pred. No.:      893      Length:      22
Score:          28.00     Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    60.87%   Indels:      0
DB:             13      Gaps:        0

US-10-023-182-6 (1-9) x US-10-431-438-14 (1-22)

QY      3 SerLeuMetTrp 7
Db      15 TCCCTCTGATGTGG 1

RESULT 14
US-09-957-667-7
; Sequence 7, Application US/09957667
; Patent No. US20020155157A1
; GENERAL INFORMATION:
; APPLICANT: LHO, DAN
; APPLICANT: MULLER, MARK
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR POLYNUCLEOTIDE DELIVERY
; FILE REFERENCE: 082035-0283695
; CURRENT APPLICATION NUMBER: US/09/957,667
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/244,722
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/074,213
; PRIOR FILING DATE: 1998-02-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-957-667-7

Alignment Scores:
Pred. No.:      937      Length:      23
Score:          28.00     Matches:      4
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 0
Query Match:    60.87%   Indels:      0
DB:             10      Gaps:        0

US-10-023-182-6 (1-9) x US-09-957-667-7 (1-23)

QY      4 LeuLeuMetTrpIleThr 9
Db      1 CTGATTCTGTGATTAACC 18

RESULT 15
US-10-098-263B-60841/C
; Sequence 60841, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
```

```
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 60841
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-60841

Alignment Scores:
Pred. No.:      1,02e+03   Length:      25
Score:          28.00     Matches:      4
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 57.14% Mismatches: 0
Query Match:    60.87%   Indels:      0
DB:             15      Gaps:        0

US-10-023-182-6 (1-9) x US-10-098-263B-60841 (1-25)

QY      3 SerLeuMetTrpIleThr 9
Db      25 ACACTTCTGATCTGTATACA 5

Search completed: February 22, 2004, 00:58:48
Job time : 217.931 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2004, 19:17:36 ; Search time 1303.14 Seconds

(without alignments)
167,857 Million cell updates/sec

Title: US-10-023-182-6
Perfect score: 46 QUSLMWIT 9
Sequence: 1 QUSLMWIT 9

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Xgapext 0.5
Xgapop 6.0 , Xgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 43814

Minimum DB seq length: 0
Maximum DB seq length: 33

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL-frame+ p2n.model -DEX=xlh
-Q=/cgn2_1/USFTO.spool/US10023182/runat.20022004.111043.21331/app.query.fasta_1.597
-DB=EST -QMT=fastcap -SUFFIX=rc -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=DIOSum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pc -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=33
-USR=US10023182 @CGN 1.1 4482 @runat.20022004.111043.21331 -NCPU=6 -ICPU=3
-NO MMAR -LARGEOUT=NEG -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEF TIMEOUT=120 MARR TIMEOUT=30 -THREAS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:
1: em_estba:
2: em_esthum:
3: em_estin:
4: em_estnu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_inco:
9: gb_est1:
10: gb_est2:
11: gb_est3:
12: gb_est4:
13: gb_est5:
14: gb_est6:
15: em_estfun:
16: em_estom:
17: em_gss_hum:
18: em_gss_inv:
19: em_gss_pln:
20: em_gss_vrt:
21: em_gss_fam:
22: em_gss_mus:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_rnd:
26: em_gss_dhg:
27: em_gss_vrt:
28: gb_gss1:

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	60.9	24	28	AZ786547
2	28	60.9	32	9	AU006847
3	27	58.7	28	29	B2384708
4	27	58.7	33	29	AL1770136
5	26	56.5	24	28	AZ309470
6	26	56.5	28	14	C00250
7	26	56.5	29	29	B2765533
8	26	56.5	32	28	AZ785127
9	26	56.5	33	14	D45809
10	25	54.3	20	28	AZ478502
11	25	54.3	23	28	AZ503299
12	25	54.3	25	29	B2765065
13	25	54.3	28	9	AA466466
14	25	54.3	28	28	AZ475208
15	25	54.3	30	28	AZ615820
16	25	54.3	32	28	AZ303920
17	24	52.2	22	28	AZ311479
18	24	52.2	22	28	AZ336549
19	24	52.2	24	28	AZ826552
20	24	52.2	28	28	AZ595788
21	24	52.2	28	29	B2286269
22	24	52.2	31	28	AZ372016
23	24	52.2	33	28	AZ766467
24	24	52.2	33	28	AZ686781
25	24	52.2	33	29	AL941403
26	23	50.0	21	28	AZ355490
27	23	50.0	23	29	TA20811P
28	23	50.0	26	29	TA128F12P
29	23	50.0	27	29	AU260098
30	23	50.0	27	28	AZ466281
31	23	50.0	28	31	A1224617
32	23	50.0	29	28	BH846837
33	23	50.0	31	14	B52745
34	23	50.0	31	28	AZ824155
35	23	50.0	32	28	AZ333224
36	23	50.0	32	28	AZ467446
37	23	50.0	32	29	BX533576
38	23	50.0	33	28	AZ666461
39	23	50.0	33	28	AZ439162
40	22	47.8	21	28	AZ655019
41	22	47.8	22	12	BH396126
42	22	47.8	22	29	TA296E05Q
43	22	47.8	23	28	AZ785457
44	22	47.8	23	28	BW396623
45	22	47.8	24	12	BW396623

ALIGNMENTS

RESULT 1
AZ786547
LOCUS 24 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0032B10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0032B10 F, genomic survey sequence.
ACCESSION AZ786547
VERSION AZ786547.1 GI:12924417
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)


```

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Baccioni, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UTM
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0032 row: B column: 10
Seq primer: CGTTGTAAACGACCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.

FEATURES
source
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="TUGC2M0032B10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid TUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/narcs/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
Chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
3 a 3 c 5 g 13 t
ORIGIN

Alignment Scores:
Pred. No.: 2,92e+03 Length: 24
Score: 28.00 Matches: 4
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 57.14% Mismatches: 0
Query Match: 60.87% Indels: 0
DB: 28 Gaps: 0

US-10-023-182-6 (1-9) X AZ786547 (1-24)
CY
2 LeuSerLeuLeuMetTrpIle 8
|||||:|||||:|||||:
2 TTAATTTGTTGCTTGGCTT 22

RESULT 2
A0006847 32 bp mRNA linear EST 31-JUL-1996
A0006847 Schizosaccharomyces pombe late log phase cDNA
DEFINITION Schizosaccharomyces pombe cDNA clone spc01028, mRNA sequence.
ACCESSION A0006847 GI:3343305
VERSION

```

```

SOURCE          EST.
ORGANISM        Schizosaccharomyces pombe (fission yeast)
                Schizosaccharomyces pombe
                Schizosaccharomycetes;
                Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                Schizosaccharomycetales; Schizosaccharomycetaceae;
                Schizosaccharomycetes.
REFERENCE       1 (bases 1 to 32)
AUTHORS        Morimyo,M. and Mita,K.
TITLE          Identification of expressed sequence tags of Schizosaccharomyces
                pombe
JOURNAL         Unpublished
COMMENT        Contact: Mitsunori Morimyo
                Genome Research Group
                National Institute of Radiological Sciences
                9-1, Anagawa-4-chome, Inage-Ku, Chiba, Chiba 263-8555, Japan
                Email: morimyo@nirs.go.jp.
FEATURES       Location/Qualifiers
                source
                1..32
                /organism="Schizosaccharomyces pombe"
                /mol_type="mRNA"
                /strain="972"
                /db_xref="taxon:4896"
                /clone="spc01028"
                /sex="h minus"
                /clone_1fb="Schizosaccharomyces pombe late log phase cDNA"
                /note="Vector: M13mp19. The cDNA library of
                Schizosaccharomyces pombe was prepared by cloning cDNA
                into the SmaI site of M13mp19 DNA and the direction of DNA
                sequences was not always from 5' to 3'. The cDNA data of
                Schizosaccharomyces pombe are available for searching on
                the World Wide Web. (URL, http://www.nirs.go.jp)"
BASE COUNT     12 a      3 c      3 g      14 t
ORIGIN
Alignment Scores:
Pred. NO.:      4.59e+03      Length:      32
Score:          28.00         Matches:      4
Percent Similarity: 100.00%   Conservative: 2
Best Local Similarity: 66.67%   Mismatches:  0
Query Match:    60.87%        Indels:      0
DB:             9            Gaps:         0
US-10-023-182-6 (1-9) x AU006847 (1-32)
Cy            4 LeuleumettTrilettr 9
              ::::::::::::::::::::
Db            11 ATACTGTTATCGATTACA 28
RESULT 3
BZ384708      28 bp      DNA      linear      GSS 26-NOV-2002
LOCUS        SALK_135903.41.95.x Arabidopsis thaliana TMA insertion lines
DEFINITION   Arabidopsis thaliana genomic clone SALK_135903.41.95.x, genomic
              survey sequence.
ACCESSION    BZ384708
VERSION      BZ384708
KEYWORDS     BZ384708.1 GI:25482406
SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; euclidocyledons; core eudicots; rosids
              1 (eucosids II; Brassicales; Brassicaceae; Arabidopsis.
              1 (bases 1 to 28)
              Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab
              ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednits,L., Shinn,P
              , Zimmerman,J. and Ecker,J.R.
              'A Sequence-Indexed Library of Insertion Mutations in the
              Arabidopsis Genome
              Unpublished
              Contact: Joseph R. Ecker
              Salk Institute Genomic Analysis Laboratory (SIGAL)
              The Salk Institute for Biological Studies
              10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

```

Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: eckert@salix.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.

FEATURES
 source
 Location/Qualifiers

1..28
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_135903.41.95.x"
 /note="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT
 ORIGIN
 14 a 8 c 2 g 4 t

Alignment Scores:
 Pred. No.: 5.63e+03 Length: 28
 Score: 27.00 Matches: 5
 Percent Similarity: 83.33% Conservative: 0
 Best Local Similarity: 83.33% Mismatches: 1
 Query Match: 58.70% Indels: 0
 DB: 29 Gaps: 0

US-10-023-182-6 (1-9) x B2384708 (1-28)

Qy 2 LeuSerLeuLeuMetTrp 7
 Db 26 CTTAGCTATTGTTTGG 9

RESULT 4
 AL770136 33 bp DNA linear GSS 19-JUN-2002
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-168C04-013363,
 DEFINITION genomic survey sequence.
 ACCESSION AL770136
 VERSION AL770136.1 GI:21532338
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
 AUTHORS Strizhov, N., Li, Y., Rosco, M., Viehoveer, P., Dekker, K., Saedler, H.
 and Weishaar, B.
 TITLE A pipeline for automated high-throughput generation of FSTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA
 transformed lines
 JOURNAL Unpublished
 REFERENCE 2
 AUTHORS Rosco, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weishaar, B.
 TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 33)
 AUTHORS Li, Y., Strizhov, N., Rosco, M. and Weishaar, B.
 TITLE Direct Submission

COMMENT Submitted (17-JUN-2002) Weishaar, B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion within the locus defined by clone T16N1.
 The sequences are generated at the MPI for Plant Breeding Research
 in the context of the GABI-Kat project. GABI-Kat is part of the
 German plant genomics program designated 'GABI'. Information on
 line availability can be found at:

http://www.mpiz-koeln.mpg.de/GABI-Kat/
 Location/Qualifiers

1..33
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-168C04-013363"
 /note="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161. The lines contain one or more T-DNA
 insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"

BASE COUNT
 ORIGIN
 6 a 10 c 7 g 10 t

Alignment Scores:
 Pred. No.: 7.29e+03 Length: 33
 Score: 27.00 Matches: 4
 Percent Similarity: 85.71% Conservative: 2
 Best Local Similarity: 57.14% Mismatches: 1
 Query Match: 58.70% Indels: 0
 DB: 29 Gaps: 0

US-10-023-182-6 (1-9) x AL770136 (1-33)

Qy 1 GlnLeuSerLeuLeuMetTrp 7
 Db 5 CAACCTTGACCTCGTTCATAGG 25

RESULT 5
 LOCUS A2309470 24 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0013J13R Mouse 10kb plasmid U00CLM library Mus musculus genomic
 clone U00CLM0013J13 R, genomic survey sequence.
 ACCESSION A2309470
 VERSION A2309470.1 GI:10350484
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weis, B.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished
 REFERENCE 1
 AUTHORS Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0013 row: J column: 13
 Seq primer: CACACAGAAACACGTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers

FEATURES
 source
 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"

/db_xref="taxon:10090"
 /clone="UUGC1M0013J13"
 /sex="Male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD29V, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/notes/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 7 c 5 g 10 t

ORIGIN

Alignment Scores:
 Pred. No.: 6,67e+03 Length: 24
 Score: 26.00 Matches: 5
 Percent Similarity: 83.33% Conservative: 0
 Best Local Similarity: 83.33% Mismatches: 1
 Query Match: 56.52% Indels: 0
 DB: 28 Gaps: 0

US-10-023-182-6 (1-9) x A2309470 (1-24)

OY 2 LeuSerLeuMetTyr 7
 |||||
 6 CTTTCTCTTCTGTGTGG 23

RESULT 6 C00250 28 bp mRNA linear EST 31-DEC-2002
 LOCUS HUMGS0005922 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
 DEFINITION sequence.
 ACCESSION C00250
 VERSION C00250.1 GI:1432480
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 28)
 Okubo,K.
 BodyMap, human gene expression database
 Unpublished
 TITLE Institute for Molecular and Cellular Biol
 JOURNAL Osaka University
 COMMENT 1-3 Yamada-oka, Suita, Osaka Pref. 565, Japan
 Tel: 06-877-5111(ex.3315)
 Email: kousaku@imcb.osaka-u.ac.jp
 We are not submitting the same cDNA sequence redundantly to DBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see: http://www.imcb.osaka-u.ac.jp/bodymap/. The sequences of the clones represented by this GS sequences is also found there.

FEATURES
 source Location/Qualifiers
 1..28
 /organism="Homo sapiens"
 /mol_type="mRNA"

/db_xref="taxon:9606"
 /dev_stage="adult"
 /clone_lib="Human adult (K.Okubo)"
 /note="One or more human adult tissue"

BASE COUNT 13 a 4 c 7 g 4 t

ORIGIN

Alignment Scores:
 Pred. No.: 8,51e+03 Length: 28
 Score: 26.00 Matches: 5
 Percent Similarity: 71.43% Conservative: 0
 Best Local Similarity: 71.43% Mismatches: 2
 Query Match: 56.52% Indels: 0
 DB: 14 Gaps: 0

US-10-023-182-6 (1-9) x C00250 (1-28)

OY 2 LeuSerLeuMetTyrIle 8
 |||||
 21 CTAGCCTTATTCTGATC 1

RESULT 7 BZ765533 29 bp DNA linear GSS 13-MAR-2003
 LOCUS SALK_131641.20.05.x Arabidopsis thaliana TDNA insertion lines
 DEFINITION Arabidopsis thaliana genomic clone SALK_131641.20.05.x, genomic survey sequence.

ACCESSION BZ765533
 VERSION BZ765533.1 GI:29938086
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadinab
 1 (bases 1 to 29)
 C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
 Zimmerman,J. and Ecker,J.R.
 A Sequence-indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL Unpublished
 CONTACT: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At3g46620.
 Class: TDNA tagged.

FEATURES
 source Location/Qualifiers
 1..29
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_131641.20.05.x"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 4 a 6 c 6 g 13 t

ORIGIN

Alignment Scores:
 Pred. No.: 8,99e+03 Length: 29
 Score: 26.00 Matches: 5
 Percent Similarity: 83.33% Conservative: 0

Best Local Similarity: 83.33% Mismatches: 1
 Query Match: 56.52% Indels: 0
 DB: 29 Gaps: 0

US-10-023-182-6 (1-9) x B276553 (1-29)

Qy 3 SerleuleuMetTrp 8
 |||||
 5 TCATTACTCCGTTGAGAT 22

RESULT 8
 AZ785127 32 bp DNA linear GSS 16-FEB-2001
 LOCUS AZ785127
 DEFINITION 2M0028115R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCG2M0028115 R, genomic survey sequence.
 ACCESSION AZ785127
 VERSION AZ785127.1 GI:12921557
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 32)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duvai, B., Hamli, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meener, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0028 row: 1 column: 15
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 32.
 Location/Qualifiers
 1..32
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0028115"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: FMD22v; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (G14732114|b|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT
 4 a 5 c 12 g 11 t

ORIGIN
 Alignment Scores:
 Pred. No.: 1.05e+04 Length: 32
 Score: 26.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 80.00% Mismatches: 0
 Query Match: 56.52% Indels: 0
 DB: 28 Gaps: 0

US-10-023-182-6 (1-9) x AZ785127 (1-32)

Qy 3 SerleuleuMetTrp 7
 |||||
 18 TCATGTTGATGTGG 32

RESULT 9
 D45809 33 bp mRNA linear EST 20-FEB-1995
 LOCUS D45809/c
 DEFINITION HMG503027 Human adult lung 3' directed Mbol cDNA Homo sapiens cDNA
 3', mRNA sequence.
 ACCESSION D45809
 VERSION D45809.1 GI:662763
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 33)
 Itoh, K., Okubo, K., Yosi, J., Yokouchi, H. and Matsubara, K.
 An expression profile of active genes in human lung
 JOURNAL DNA Res. 1, 279-287 (1994)
 MEDLINE 95236275
 PUBMED 7719923
 COMMENT Contact: Kohichi Itoh
 Institute for Molecular and Cellular Biology
 Osaka University
 3-1, Yamadaoka, Suita, Osaka, 565, Japan
 Tel: 06-877-5111 x3910
 Fax: 06-877-1922.
 Location/Qualifiers
 1..33
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_1lb="Human adult lung 3' directed Mbol"
 /note="Adult human lung, 3' directed Mbol"

BASE COUNT
 13 a 10 c 3 g 7 t

ORIGIN
 Alignment Scores:
 Pred. No.: 1.1e+04 Length: 33
 Score: 26.00 Matches: 4
 Percent Similarity: 83.33% Conservative: 1
 Best Local Similarity: 66.67% Mismatches: 1
 Query Match: 56.52% Indels: 0
 DB: 14 Gaps: 0

US-10-023-182-6 (1-9) x D45809 (1-33)

Qy 2 LeuSerleuMetTrp 7
 |||||
 22 ATTAGTTATTCATGTGG 5

RESULT 10
 AZ478502 20 bp DNA linear GSS 04-OCT-2000
 LOCUS AZ478502
 DEFINITION 1M0298909R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCG1M0298909 R, genomic survey sequence.
 ACCESSION AZ478502
 VERSION AZ478502.1 GI:10637408
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0298 row: B column: 09
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0298B05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 3 a 5 c 5 g 7 t
ORIGIN

Alignment Scores:
Pred. No.: 7,57e+03 Length: 20
Score: 25.00 Matches: 3
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 60.00% Mismatches: 0
Query Match: 54.35% Indels: 0
DB: 28 Gaps: 0

US-10-023-182-6 (1-9) x AZ478502 (1-20)

QY 5 LeuMetTIpIleThr 9
|||||:|||||
DB 3 TTGCTTTGGGTAC 17

RESULT 11
AZ503299 23 bp DNA 1linear GSS 05-OCT-2000
LOCUS 6

DEFINITION 1M0343D05F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0343D05 F, genomic survey sequence.
ACCESSION
VERSION AZ503299
AZ503299.1 GI:10684615

KEYWORDS GSS
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0343 row: D column: 05
Seq primer: CGTTGTAAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0343D05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 5 a 3 c 4 g 11 t
ORIGIN

Alignment Scores:
Pred. No.: 9,43e+03 Length: 23
Score: 25.00 Matches: 5
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 54.35% Indels: 0
DB: 28 Gaps: 0

US-10-023-182-6 (1-9) x AZ503299 (1-23)

QY 1 GlnIeuSerIeuIeuMetTIp 7

Db 2 CAGTATCTTATGCTTAT 22

RESULT 12
BZ765065 25 bp DNA linear GSS 13-MAR-2003
LOCUS SALK_128228.43.60.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_128228.43.60.x, genomic survey sequence.

ACCESSION BZ765065
VERSION BZ765065.1 GI:28937618
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosid II; Brassicales; Brassicaceae; Arabidopsi
s.
1 (bases 1 to 25)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab
, C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
, Zimmerman,J. and Ecker,J.R.
A Sequence-indexed library of Insertion Mutations in the
Arabidopsis Genome
Unpublished
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At5g23940.
Class: TDNA tagged.
Location/Qualifiers
1..25
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_128228.43.60.x"
/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 6 a 3 c 7 g 9 t

ORIGIN

Alignment Scores:
Pred. No.: 1.08e+04 Length: 25
Score: 25.00 Matches: 4
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 54.35% Indels: 0
DB: 29 Gaps: 0

US-10-023-182-6 (1-9) x BZ765065 (1-25)

QY 2 LeuSerLeuMetTyr 7
1 TTGAAGCTCTCTGTTATG 18

Db

RESULT 13
AA466466 28 bp mRNA linear EST 11-JUN-1997
LOCUS AA466466
DEFINITION Y887305.11 Barstead mouse pooled organs MRLR84 Mus musculus cDNA
clone IMAGE:872937 5' similar to TR:G205858 G205858 RAT ORF,
COMPLETE CDS. //, mRNA sequence.

ACCESSION AA466466
VERSION AA466466.1 GI:2192606

KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Marra,M., Haller,U., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Stepec,M., Tan,F., Underwood,K., Moore,B.,
Weinstein,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:512417
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28mt3 rev2 RT from Amersham
High quality sequence, stop: 1.
Location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:872937"
/sex="mixed"
/tissue_type="pooled organs"
/dev_stage="7 day"
/lab_host="DH10B"
/clone_lib="Barstead mouse pooled organs MRLR84".
/note="Organ: pooled. Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACGATCTGAGGAGGAGCGCCCTTTTCTTTTCTTTTCTTTT
3']"; double-stranded cDNA was ligated to Eco RI adaptors
(GTGATTCGATCC), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library constructed by Bob Barstead."

BASE COUNT 2 a 8 c 8 g 9 t

ORIGIN

Alignment Scores:
Pred. No.: 1.29e+04 Length: 28
Score: 25.00 Matches: 4
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 80.00% Mismatches: 0
Query Match: 54.35% Indels: 0
DB: 9 Gaps: 0

US-10-023-182-6 (1-9) x AA466466 (1-28)

QY 3 SerLeuLeuMetTyr 7
14 GCNCTTCATGATGG 28

Db

RESULT 14
AZ475208 28 bp DNA linear GSS 04-OCT-2000
LOCUS AZ475208
DEFINITION IM0293318F Mouse 10kb plasmid UUCGM library Mus musculus genomic
clone UUCGM0293318 F, genomic survey sequence.

ACCESSION AZ475208
VERSION AZ475208.1 GI:10633333
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

```

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (base 1 to 28)

REFERENCE
Dunn,D., Aoyagi,A., Barber,M., Baacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenan,B., Pedersen,T., Rellly
,M., Rose,M., Rose,R., Stokes,R., Tinige,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE
Unpublished

JOURNAL
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0293 row: B column: 18
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers

FEATURES
Source
1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0293E18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U06C1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/nmres/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 [g14732114[gblAF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
13 a 7 c 3 g 5 t

ORIGIN
Alignment Scores:
Pred. No.: 1.29e+04 Length: 28
Score: 25.00 Matches: 3
Percent Similarity: 83.33% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 54.35% Indels: 0
Gaps: 0

US-10-023-182-6 (1-9) x AZ475208 (1-28)

cy 4 LeuMetTrpIleThr 9
|||::|::|::|::|
DB 22 CTTTATTATGGCTACA 5

RESULT 15
AZ615820 30 bp DNA linear GSS 13-DEC-2000
AZ615820

```

```

DEFINITION      IM0445A21F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
VERSION         A2615820
KEYWORDS        A2615820.1  GI:11738010
SOURCE          GSS.
ORGANISM        Mus musculus (house mouse)
AUTHORS         Mus musculus
REFERENCE       1 (bases 1 to 30)
                Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Idlam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
                ,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
                and Wright,D., Weiser,R.
                Mouse whole genome scaffolding with paired end reads from 10kb
                Plasmid inserts
TITLE           Unpublished
COMMENT         Contact: Robert B. Weiss
                University of Utah Genome Center
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel.: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000  Std Error: 0.00
                Plate: 0445  row: A  column: 21
                Seq primer: CGTTGTAAACGACGCGCCAGT
                Class: plasmid ends
                High quality sequence stop: 30.
FEATURES
    source
        1..30
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGCIM0445A21"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
            /clone_id="Mouse 10kb plasmid UUGCIM library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PWD42 (G1|473114|gb|AF129072.1|), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
BASE COUNT      7 a          9 c          3 g          11 t
ORIGIN
Alignment Scores:
Pred. No.:      1,43e+04      Length:      30
Score:          25.00         Matches:      5
Percent Similarity: 71.43%    Conservative: 0
Best Local Similarity: 71.43% Mismatches:      2
Query Match:    54.35%       Indels:        0
DB:             28           Gaps:         0

```

Mon Feb 23 07:48:09 2004

us-10-023-182-6.rst

Page 9

Db 6 CTTCAITGCTCATGATT 26

Search completed: February 21, 2004, 22:51:42
Job time : 1305.14 secs